

SEQUENCE LISTING

<110> Wagner, et al.

<120> GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM

<130> 1505-54357

<140> 09/513,057

<141> 2000-02-24

<160> 68

<170> PatentIn version 3.1

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Gln Ala Asn Glu Gln Thr Asn Gln Phe Gly Tyr Ser Gly Asn Leu Gln															
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645 650															

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 35 40 45

Phe Gly Asp His Gly Asn Leu Ser Leu Ser Ser Arg Ser Asn Asn Thr
 50 55 60

Ser Thr Leu Val His Pro Gly Pro Ser Asn Gln Gln Ser Cys Gly Val
 65 70 75 80

Glu Arg Asn Leu Ser Val Gln His Leu Asp Ser Ser Ala Ala Val His
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Val Thr Glu Asn Phe Val Ser Gln Met Pro Phe Met Glu Asn Met Arg
 100 105 110

Ser Leu Ala Lys His Asp Gln Arg Lys Thr Val Arg Glu Glu Asp Asp
 115 120 125

Phe Ala Val Pro Val Phe Val Asn Ser Arg Arg Phe Gln Ser His Gly
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Ser Thr Lys Ser Gly Ile Val Ile Glu Lys His Thr Thr Leu Ala Thr
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Cys Ser Lys Leu Val Arg Asp Lys Val Lys Met Asn Ala Lys Ser Gly
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Gly Phe Ile Asp Leu Ser Ser Thr Glu Glu Val Asp Leu Glu Lys Ser
 180 185 190

Ala Ser Ser Tyr Asp Arg Val Asn Asp Cys Asn Ser Ser Leu Arg Gln
195 200 205

Glu Ser Arg Asn Lys Leu Tyr Arg Asp Gly Gly Glu Ala His Met Lys
210 215 220

Asp Thr Ala Asn Arg Val Glu Ser His Leu Val Thr Glu Ser His Ser
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Glu Glu Gly His Gly Ser Pro Asp Asp Asp Asn Gly His Glu Tyr
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Cys Arg Ser Arg Gly Gly Val Ser Leu Gln Gln Ile Asn Glu Glu Ala
260 265 270

Ser Asp Asp Val Ser Asp Asn Ser Met Val Asp Ser Ile Ser Ser Ile
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Asp Val Ser Pro Asp Asp Val Val Gly Ala Leu Gly Gln Lys Arg Phe
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Trp Arg Ala Arg Lys Ala Ile Thr Asn Gln Gln Arg Val Phe Ala Val
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Gln Leu Phe Glu Leu His Arg Leu Ile Lys Val Gln Arg Leu Ile Ala
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Ala Ser Pro Asp Ile Val Leu Asp Glu Ile Asn Tyr Leu Gly Lys Val
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Ser Ala Lys Ser Tyr Pro Val Lys Lys Leu Val Pro Ser Glu Phe Ile
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Val Val Gly Arg Leu Ser Asn Gln Gly His His His Asn His Gln Pro
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Ser Asn Tyr Met Pro Phe Pro Ser Asn Pro Pro Ala Ser Pro Ala Val

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Asn Gly Cys Cys Tyr Pro Pro Gln Pro Pro Pro Ser Gly Asn Gln Gln	435	440		445
Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Ile Tyr Lys Pro	450	455		460
His Pro Gly Met Gly His Thr Gly His Tyr Gly Gly Tyr Tyr Gly His	465	470	475	480
Phe Met Pro Pro Pro Met Val Met Pro Pro Phe His Pro Gly Met Gly	485	490		495
Phe Pro Pro Pro Gly Asn Gly Tyr Phe Pro Pro Tyr Gly Val Ile Pro	500	505		510
Ala Met Met Asn Pro Tyr Gly Pro Gly Gln Gln Gln Gln Gln Gln Pro	515	520	525	
Gln Ala Asn Glu Gln Thr Asn Gln Phe Gly Tyr Ser Gly Asn Leu Gln	530	535	540	
Asn Asn Thr His Gln Glu Ser Ser Val Asn Glu Ala Ala Pro Pro Gln	545	550	555	560
Glu Pro Leu Thr Lys Ser Tyr Pro Arg Ala Arg Lys Ser Arg Gln Val	565	570		575
Ser Thr Ala Ser Ser Ala Ser Gly Arg Glu Gly Ile Ser Gly Ser Thr	580	585	590	
Ser Phe Arg Pro Phe Ser Ala Val Asp Glu Asp Asn Asn Asp Asn Asn	595	600	605	
Asn Asp Ala Pro Asp Gln Met Met Thr Thr Thr Thr Thr Thr Arg	610	615	620	
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ggtgggtcaat tagtgggttt tgttttgagt ttcatttgat ttgtgggttt agttttttga 180

agcttattgt tacgaaattt tgggtctttt tcaatttttag gtcaaataat tggggaaaag 240

ttgagaaatc gtgtgaaatt aggttatttg ggttgagaaa ttttgaagca aagtttgtga 300

gttgtg atg aag aga ggg aaa gat gat gag aag ata ctg gaa cct atg 348

Met Lys Arg Gly Lys Asp Asp Glu Lys Ile Leu Glu Pro Met
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ttt cct aga ctt cat gtg aat gat gca gat aaa gga gga cct aga gct 396

Phe Pro Arg Leu His Val Asn Asp Ala Asp Lys Gly Gly Pro Arg Ala
15 20 25 30

cct cct aga aac aag atg gct ctt tat gag cag ctt agt atc cct tct 444

Pro Pro Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser
35 40 45

gag agg ttt ggt gat cat gga aat ttg tct ctg agt tct cgt agt aac	492
Glu Arg Phe Gly Asp His Gly Asn Leu Ser Leu Ser Ser Arg Ser Asn	
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Asn Thr Ser Thr Leu Val His Pro Gly Pro Ser Asn Gln	
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Gln Ser Cys Gly Val Glu	
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Thr Glu Asn Phe Val Ser Gln Met Pro Phe Met Glu Asn Met Arg Ser	
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Leu Ala Lys His Asp Gln Arg Lys Thr Val Arg Glu Glu Asp Asp Phe	
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Ala Val Pro Val Phe Val Asn Ser Arg Arg Phe Gln Ser His Gly Ser	
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Thr Lys Ser Gly Ile Val Ile Glu Lys His Thr Thr Leu Ala Thr Cys	
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Ser Lys Leu Val Arg Asp Lys Val Lys Met Asn Ala Lys Ser Gly Gly	
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Phe Ile Asp Leu Ser Ser Thr Glu Glu Val Asp Leu Glu Lys Ser Ala	
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Ser Ser Tyr Asp Arg Val Asn Asp Cys Asn Ser Ser Leu Arg Gln Glu	
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Arg Val Phe Ala Val Gln Leu Phe Glu Leu His Arg Leu Ile Lys	
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Val Gln Arg Leu Ile Ala Ala Ser Pro	
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Lys Thr Asp Gln His Lys Met Glu Cys Ser Ala Glu Asn Val Val Gly	
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Arg Leu Ser Asn Gln Gly His His His Asn His Gln Pro Ser Asn Tyr	
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Cys Tyr Pro Pro Gln Pro Pro Pro Ser Gly Asn Gln Gln Trp Leu Ile	
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Met Gly His Thr Gly His Tyr Gly Gly Tyr Tyr Gly His Phe Met Pro	
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Pro Gly Asn Gly Tyr Phe Pro Pro Tyr Gly Val Ile Pro Ala Met Met	
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His Gln Glu Ser Ser Val Asn Glu Ala Ala Pro Pro Gln Glu Pro Leu	
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 Val Gln Gln Leu Ile
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 Ala Gly Ser Pro Asp Leu Leu Phe Asp Asp Gly Ala Phe Leu Gly Lys
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 Ser Leu Pro Asp Gly Ser Thr Pro Lys Lys Leu Ser Leu Glu Tyr Val
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gta aaa gct cgg cta caa aat ctt aag cgc aaa gtt gat tct gaa aag 253
 Val Lys Ala Arg Leu Gln Asn Leu Lys Arg Lys Val Asp Ser Glu Lys
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Leu Lys Arg Lys Val Asp Ser Glu Lys Ile Asn Gln Asn Met Glu Cys
 50 55 60

Ser Ala Glu Asn Ala Val Gly Lys Thr Ser Ile Ser Ser Val Lys Asn
 65 70 75 80

Thr Ser His Leu Ser Ser Ser Met Pro Phe Ala Gly Asn Pro His Gln
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Gly Asn Val Ala Ala Asp Asn Gly Met Gly Pro Trp Cys Phe Asn Gln
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Ser Pro Gly His
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Glu Asn Gln Lys Pro Val Thr Glu Ala Tyr Pro Glu His Met Lys Pro
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Lys Ile Pro Leu Pro Phe Ile Ser Lys Glu Leu Met Thr Pro Ile Trp
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Gln Gln Gln Leu Leu Pro Pro Gln Glu Asn
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Ala Ser His Thr Tyr Phe Ala Pro Phe Gly Met Pro Val Met Asn Gln
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Ala Thr Ser Gly Ser Ala Val Glu Gln Val Asn Gln Phe Ala Ala Gln
 50 55 60

Gly Ser His Gly Gln Asn Gly His Ser Ser Val Glu Gly Ala Asp Phe
 65 70 75 80

Asn Thr His His Asn Gln Ser Ser Ser Asn Leu Pro Val Gln Lys Asn
 85 90 95

Gly Ala Arg Leu His Val Lys Lys Ser Gln Ala Leu Lys Glu Arg Gly
 100 105 110

Leu Gln Gly Ser Thr Arg Ser Ser Pro Ser Glu Met Ala Gln Gly Ile
 115 120 125

Arg Ala Arg Lys Ile Ala Asp Gly Ser Asp Ala Gln Ser Leu Ser Leu

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tttaggtggg gtttgcttg ttttcttcaa ttttgattgg ttttgttgaa aagttcagaa	300
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gttttttttg tttaatttaa tgaatgttgg agattgggtg aacctgttga gaagctatta	420
aagggaagaa atgaagagag gaaaggggtg agagaagttg atgggacctg tgtttccaag	480
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Thr Gly Glu Glu Lys Val Met Gly Pro Met Phe Pro Arg Leu Asn Val
5 10 15 20

aat gat aca gaa aaa gga ggt cca aga gca cct cca agg aac aag atg 151
Asn Asp Thr Glu Lys Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met
25 30 35

gct ctt tat gaa caa ctg agt atc cct tcc caa cga tac aac cct ggt 199
Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln Arg Tyr Asn Pro Gly
40 45 50

gat ttg cct cat aac agt agt aac agt gca aat ttg gtc ctt cct cac 247
Asp Leu Pro His Asn Ser Ser Asn Ser Ala Asn Leu Val Leu Pro His
55 60 65

cca agc cag gag aat gaa cac gaa aga ggt gta tta ttc tct aga caa 295
Pro Ser Gln Glu Asn Glu His Glu Arg Gly Val Leu Phe Ser Arg Gln
70 75 80

ctt cct gca tta aga cat cca gtt gaa aag cca tat gga cgt agt tct 343
Leu Pro Ala Leu Arg His Pro Val Glu Lys Pro Tyr Gly Arg Ser Ser
85 90 95 100

ggg tca aat act cca ttg cgg gaa gtt aag tct aaa agg cag aca gaa 391
Gly Ser Asn Thr Pro Leu Arg Glu Val Lys Ser Lys Arg Gln Thr Glu
105 110 115

aag gaa gat ttt aga gtt ccc act ttt gat aac tcc aag gag cgt gca 439
Lys Glu Asp Phe Arg Val Pro Thr Phe Asp Asn Ser Lys Glu Arg Ala
120 125 130

gta aac aca gag gac tat tct aaa ggt acc tca gat ata gat aag cga 487
Val Asn Thr Glu Asp Tyr Ser Lys Gly Thr Ser Asp Ile Asp Lys Arg
135 140 145

gac agt act ttg aag cgg act gat caa ctc tcc cat gtc aca ccg aga 535
Asp Ser Thr Leu Lys Arg Thr Asp Gln Leu Ser His Val Thr Pro Arg
150 155 160

gag aat ctt gtt aat acc ttt ggt gaa tca cat aag acc aat ata gt 582
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165 170 175

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 tct gga aca gac atc tct cct gat gac att gta gga ata att ggc tta 97
 Ser Gly Thr Asp Ile Ser Pro Asp Asp Ile Val Gly Ile Ile Gly Leu
 20 25 30
 aag cgt ttc tgg aaa gcc aga aga gca att gtc aac cag caa aga gtg 145
 Lys Arg Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln Arg Val
 35 40 45
 ttt gca atc caa gtg ttc gag ttg cat cga cta ata aag gta caa agg 193
 Phe Ala Ile Gln Val Phe Glu Leu His Arg Leu Ile Lys Val Gln Arg
 50 55 60
 ctc att gcc ggg tca cca aat agt tgc ctc gaa gat cct gct tat tta 241
 Leu Ile Ala Gly Ser Pro Asn Ser Ser Leu Glu Asp Pro Ala Tyr Leu
 65 70 75 80
 ggc aaa cct tta aag agt tca tgc atc aaa aga ctt cca ttg gac tgt 289
 Gly Lys Pro Leu Lys Ser Ser Ser Ile Lys Arg Leu Pro Leu Asp Cys
 85 90 95
 att gtt aga gaa tct caa agt gtt ctg aag cgc aag cat gat tct gag 337
 Ile Val Arg Glu Ser Gln Ser Val Leu Lys Arg Lys His Asp Ser Glu
 100 105 110
 aag cct cac ttc agg atg gaa cac act gcc gaa agc aat gtg gga aag 385
 Lys Pro His Phe Arg Met Glu His Thr Ala Glu Ser Asn Val Gly Lys
 115 120 125
 gca tct ctc tct act gtg caa aat ggt agt caa ctc tct agc cac aaa 433
 Ala Ser Leu Ser Thr Val Gln Asn Gly Ser Gln Leu Ser Ser His Lys
 130 135 140
 cca ttt tca gga act cca ctg cct aca cct gta aca aat gat tct aat 481
 Pro Phe Ser Gly Thr Pro Leu Pro Thr Pro Val Thr Asn Asp Ser Asn
 145 150 155 160
 gcg ggt cct tgg tgc ttc caa caa cct tcc ggg cac caa tgg ttg atc 529
 Ala Gly Pro Trp Cys Phe Gln Gln Pro Ser Gly His Gln Trp Leu Ile
 165 170 175

cca gtg atg tct cct tct gag gga ctt gta tac aag cca ttt tct gga Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr Lys Pro Phe Ser Gly 180 185 190	577
cct gga ttc acg agt cct att tgt gga agt ggg cct tca gga tcg agt Pro Gly Phe Thr Ser Pro Ile Cys Gly Ser Gly Pro Ser Gly Ser Ser 195 200 205	625
cca aca atg ggg aac ttt ttt gct cca aca tat gga gtt cct gct cct Pro Thr Met Gly Asn Phe Phe Ala Pro Thr Tyr Gly Val Pro Ala Pro 210 215 220	673
aat cct cac tat caa ggt atg gga gtt cct ttt gca cct ccg act ggt Asn Pro His Tyr Gln Gly Met Gly Val Pro Phe Ala Pro Pro Thr Gly 225 230 235 240	721
cat ggt tac ttt cgg caa tat ggc atg cca gct atg aat cca cca att His Gly Tyr Phe Arg Gln Tyr Gly Met Pro Ala Met Asn Pro Pro Ile 245 250 255	769
tca tca act gct agt gaa gaa tcg aac cag tat acc atg cct ggt tta Ser Ser Thr Ala Ser Glu Glu Ser Asn Gln Tyr Thr Met Pro Gly Leu 260 265 270	817
caa cac cag ttt tct gga gta gtt gat gac gtt caa cat tca aca tca Gln His Gln Phe Ser Gly Val Val Asp Asp Val Gln His Ser Thr Ser 275 280 285	865
gga ctc agt aat gtt cta aat cag aag aaa gaa aat gtc ccg gat gtt Gly Leu Ser Asn Val Leu Asn Gln Lys Lys Glu Asn Val Pro Asp Val 290 295 300	913
gta agg tat caa tcc aca aaa gat aat gag gta caa gcc agc agt gca Val Arg Tyr Gln Ser Thr Lys Asp Asn Glu Val Gln Ala Ser Ser Ala 305 310 315 320	961
agt agt cct att gag aca gca gga aga aac atg ctc tct ctt ttt ccc Ser Ser Pro Ile Glu Thr Ala Gly Arg Asn Met Leu Ser Leu Phe Pro 325 330 335	1009
acg tct cca gtt act gac aac cgt gat ggt agc cct cag gct tgt gtg Thr Ser Pro Val Thr Asp Asn Arg Asp Gly Ser Pro Gln Ala Cys Val 340 345 350	1057
cct gat aat cca gcc aga gtt atc aag gtt gta cct cac aat gca agg Pro Asp Asn Pro Ala Arg Val Ile Lys Val Val Pro His Asn Ala Arg 355 360 365	1105
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aga aat aat atg act tag gtttaacaca tctataagta gcttaccttg Arg Asn Asn Met Thr 385	1201
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<212> PRT

<213> Lycopersicon esculentum

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35 40 45

Phe Ala Ile Gln Val Phe Glu Leu His Arg Leu Ile Lys Val Gln Arg
50 55 60

Leu Ile Ala Gly Ser Pro Asn Ser Ser Leu Glu Asp Pro Ala Tyr Leu
65 70 75 80

Gly Lys Pro Leu Lys Ser Ser Ser Ile Lys Arg Leu Pro Leu Asp Cys
85 90 95

Ile Val Arg Glu Ser Gln Ser Val Leu Lys Arg Lys His Asp Ser Glu
100 105 110

Lys Pro His Phe Arg Met Glu His Thr Ala Glu Ser Asn Val Gly Lys
115 120 125

Ala Ser Leu Ser Thr Val Gln Asn Gly Ser Gln Leu Ser Ser His Lys
130 135 140

Pro Phe Ser Gly Thr Pro Leu Pro Thr Pro Val Thr Asn Asp Ser Asn
145 150 155 160

Ala Gly Pro Trp Cys Phe Gln Gln Pro Ser Gly His Gln Trp Leu Ile
165 170 175

Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr Lys Pro Phe Ser Gly
 180 185 190

Pro Gly Phe Thr Ser Pro Ile Cys Gly Ser Gly Pro Ser Gly Ser Ser
 195 200 205

Pro Thr Met Gly Asn Phe Phe Ala Pro Thr Tyr Gly Val Pro Ala Pro
 210 215 220

Asn Pro His Tyr Gln Gly Met Gly Val Pro Phe Ala Pro Pro Thr Gly
 225 230 235 240

His Gly Tyr Phe Arg Gln Tyr Gly Met Pro Ala Met Asn Pro Pro Ile
 245 250 255

Ser Ser Thr Ala Ser Glu Glu Ser Asn Gln Tyr Thr Met Pro Gly Leu
 260 265 270

Gln His Gln Phe Ser Gly Val Val Asp Asp Val Gln His Ser Thr Ser
 275 280 285

Gly Leu Ser Asn Val Leu Asn Gln Lys Lys Glu Asn Val Pro Asp Val
 290 295 300

Val Arg Tyr Gln Ser Thr Lys Asp Asn Glu Val Gln Ala Ser Ser Ala
 305 310 315 320

Ser Ser Pro Ile Glu Thr Ala Gly Arg Asn Met Leu Ser Leu Phe Pro
 325 330 335

Thr Ser Pro Val Thr Asp Asn Arg Asp Gly Ser Pro Gln Ala Cys Val
 340 345 350

Pro Asp Asn Pro Ala Arg Val Ile Lys Val Val Pro His Asn Ala Arg
 355 360 365

Ser Ala Thr Glu Ser Val Ala Arg Ile Phe Gln Ser Ile Gln Gln Glu
 370 375 380

Arg Asn Asn Met Thr
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<210> 24

<211> 179
 <212> PRT
 <213> Lycopersicon esculentum

<400> 24

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Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln Arg
 35 40 45

Tyr Asn Pro Gly Asp Leu Pro His Asn Ser Ser Asn Ser Ala Asn Leu
 50 55 60

Val Leu Pro His Pro Ser Gln Glu Asn Glu His Glu Arg Gly Val Leu
 65 70 75 80

Phe Ser Arg Gln Leu Pro Ala Leu Arg His Pro Val Glu Lys Pro Tyr
 85 90 95

Gly Arg Ser Ser Gly Ser Asn Thr Pro Leu Arg Glu Val Lys Ser Lys
 100 105 110

Arg Gln Thr Glu Lys Glu Asp Phe Arg Val Pro Thr Phe Asp Asn Ser
 115 120 125

Lys Glu Arg Ala Val Asn Thr Glu Asp Tyr Ser Lys Gly Thr Ser Asp
 130 135 140

Ile Asp Lys Arg Asp Ser Thr Leu Lys Arg Thr Asp Gln Leu Ser His
 145 150 155 160

Val Thr Pro Arg Glu Asn Leu Val Asn Thr Phe Gly Glu Ser His Lys
 165 170 175

Thr Asn Ile

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<213> Lycopersicon esculentum

<400> 25

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Phe

<210> 26

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 Gly Lys Val Met Gly Pro Leu Phe Pro Arg Leu His Val Asn Asp Ala
 20 25 30
 gcc aag ggc gga ggc ccg cgg gcg ccg ccc cgg aac aag atg gcg ctc 144
 Ala Lys Gly Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met Ala Leu
 35 40 45
 tac gag cag ttc acc gtg ccc tcg cat cgc ttc agc ggc gga gga ggc 192
 Tyr Glu Gln Phe Thr Val Pro Ser His Arg Phe Ser Gly Gly Gly Gly
 50 55 60
 ggc ggc gga gta gga ggc agc ccc gcg cac tcg acg tcg gcg gcg agc 240
 Gly Gly Gly Val Gly Gly Ser Pro Ala His Ser Thr Ser Ala Ala Ser
 65 70 75 80
 cag agc cag agc cag agc cag gtgactcgac gtcctgcccg tatgatcgat 291
 Gln Ser Gln Ser Gln Ser Gln
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	Val Tyr Gly 90
cgt gac agt tct ctg ttc cag ccg ttc aat gtg cct tcc aat cga cct	1716
Arg Asp Ser Ser Leu Phe Gln Pro Phe Asn Val Pro Ser Asn Arg Pro	95 100 105
ggc cat tct act gaa aag atc aat tca gat aag atc aac aag aag att	1764
Gly His Ser Thr Glu Lys Ile Asn Ser Asp Lys Ile Asn Lys Lys Ile	110 115 120
agt ggt tca aga aaa gaa ctg ggg atg tta tcc tct cag act aag ggc	1812
Ser Gly Ser Arg Lys Glu Leu Gly Met Leu Ser Ser Gln Thr Lys Gly	125 130 135
atg gat att tat gct tca aga tca act gct gag gca cca caa aga aga	1860
Met Asp Ile Tyr Ala Ser Arg Ser Thr Ala Glu Ala Pro Gln Arg Arg	140 145 150
gca gaa aat aca ata aag agt tct tcg gga aag aga ttg gcc gat gat	1908
Ala Glu Asn Thr Ile Lys Ser Ser Ser Gly Lys Arg Leu Ala Asp Asp	155 160 165 170
gat gaa ttt atg gtt cct tct gtc ttc aat tcc aga ttt cct caa tat	1956
Asp Glu Phe Met Val Pro Ser Val Phe Asn Ser Arg Phe Pro Gln Tyr	175 180 185
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Ser Thr Gln Glu Asn Ala Gly Val Gln Asp Gln Ser Thr Pro Leu Val	190 195 200
gct gca aat cca cac aaa agc cct tca aca gtg tcc aaa tca tcc aca	2052
Ala Ala Asn Pro His Lys Ser Pro Ser Thr Val Ser Lys Ser Ser Thr	205 210 215

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tcc aaa gat atg ttt gaa agc agg cat gct aaa gta tat cct aag atg Ser Lys Asp Met Phe Glu Ser Arg His Ala Lys Val Tyr Pro Lys Met 270 275 280	2244
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aat act gat agg cat tat aat tta ccg caa gga ggc ata gag gaa aca Asn Thr Asp Arg His Tyr Asn Leu Pro Gln Gly Gly Ile Glu Glu Thr 335 340 345	2436
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ctgtatgatt ccctttattg ttttacactc taatcttctt taaactctat gcag t caa	3333
	Gln
cag agg gtg ttt gct gtc cag gtt ttt gag ctg cat aag ttg gta aaa	3381
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gattttgtcc ataatctgtt tataaccac acttgtattt gacttacaat cag gtg	3497
	Val
cag aag ttg att gca gca tgc cca cat gta ctt att gaa agt gat cct	3545
Gln Lys Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Ser Asp Pro	
435 440 445 450	
tgc ctt ggc aat gcc ttg ttg ggt agc aag aac aag ctg gtg gaa gaa	3593
Cys Leu Gly Asn Ala Leu Leu Gly Ser Lys Asn Lys Leu Val Glu Glu	
455 460 465	
aac ctg aaa gca caa cct ctt tta gtc gca acc atc gat gac gtg gag	3641
Asn Leu Lys Ala Gln Pro Leu Leu Val Ala Thr Ile Asp Asp Val Glu	
470 475 480	
cca agt cta cag caa ccg gag gta tca aaa gaa aac act gaa gac agc	3689
Pro Ser Leu Gln Gln Pro Glu Val Ser Lys Glu Asn Thr Glu Asp Ser	
485 490 495	
cca ccc tcc cct cat gat act ggg ctt ggc agt ggt caa cgt gat caa	3737
Pro Pro Ser Pro His Asp Thr Gly Leu Gly Ser Gly Gln Arg Asp Gln	
500 505 510	
gct gca aca aat ggc gtc tct aaa agc aat cgt cga gct aca cct gtt	3785
Ala Ala Thr Asn Gly Val Ser Lys Ser Asn Arg Arg Ala Thr Pro Val	
515 520 525 530	
gct tct gat aac aaa caa aat aac tgg ggc gtt caa ctt caa cca cct	3833
Ala Ser Asp Asn Lys Gln Asn Asn Trp Gly Val Gln Leu Gln Pro Pro	
535 540 545	

caa aat caa tgg ctt gtc cct gtc atg tct cct ttg gaa ggc ctt gtc	3881
Gln Asn Gln Trp Leu Val Pro Val Met Ser Pro Leu Glu Gly Leu Val	
550 555 560	
tat aag cct tat tct ggt ccg tgc cct cca gct ggt agc ata ttg gcc	3929
Tyr Lys Pro Tyr Ser Gly Pro Cys Pro Pro Ala Gly Ser Ile Leu Ala	
565 570 575	
ccg ttt tat gcc aac tgt act cct ttg agt ctt cca tca aca gct gga	3977
Pro Phe Tyr Ala Asn Cys Thr Pro Leu Ser Leu Pro Ser Thr Ala Gly	
580 585 590	
gat ttc atg aac tcg gca tac ggt gtt cct atg cct cat cag cca caa	4025
Asp Phe Met Asn Ser Ala Tyr Gly Val Pro Met Pro His Gln Pro Gln	
595 600 605 610	
cat atg ggt gct cct ggc cct cct tcc atg cct atg aac tac ttc ccg	4073
His Met Gly Ala Pro Gly Pro Pro Ser Met Pro Met Asn Tyr Phe Pro	
615 620 625	
cct ttc agc ata cca gtg atg aac cca act gca ccg gca cct gta gtc	4121
Pro Phe Ser Ile Pro Val Met Asn Pro Thr Ala Pro Ala Pro Val Val	
630 635 640	
gaa caa ggg aga cat cct tcg atg cca cag cct tat ggg aac ttt gag	4169
Glu Gln Gly Arg His Pro Ser Met Pro Gln Pro Tyr Gly Asn Phe Glu	
645 650 655	
cag cag tcg tgg atc tca tgt aac atg tca cat cca agt ggc att tgg	4217
Gln Gln Ser Trp Ile Ser Cys Asn Met Ser His Pro Ser Gly Ile Trp	
660 665 670	
aga ttt cat gcc tca aga gat agc gag gca cag gcc agc agc gct agc	4265
Arg Phe His Ala Ser Arg Asp Ser Glu Ala Gln Ala Ser Ser Ala Ser	
675 680 685 690	
agt cct ttt gac agg ttc caa tgc agt gga agt ggt cct gta tcc gcc	4313
Ser Pro Phe Asp Arg Phe Gln Cys Ser Gly Ser Gly Pro Val Ser Ala	
695 700 705	
ttc ccc aca gta tca gct cag aac aac cag cct cag ccc tca tat agc	4361
Phe Pro Thr Val Ser Ala Gln Asn Asn Gln Pro Gln Pro Ser Tyr Ser	
710 715 720	
agc cgg gac aac cag acc aat gtt atc aag gtt gtt cca cat aat tca	4409
Ser Arg Asp Asn Gln Thr Asn Val Ile Lys Val Val Pro His Asn Ser	
725 730 735	
cga act gct tca gag tca gca gca cgg att ttc cgg tca ata caa atg	4457
Arg Thr Ala Ser Glu Ser Ala Ala Arg Ile Phe Arg Ser Ile Gln Met	
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gaa cgg caa cga gat gat tga	4478
Glu Arg Gln Arg Asp Asp	
755 760	

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 <213> Oryza sativa

<400> 27

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Gly Lys Val Met Gly Pro Leu Phe Pro Arg Leu His Val Asn Asp Ala
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Ala Lys Gly Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met Ala Leu
 35 40 45

Tyr Glu Gln Phe Thr Val Pro Ser His Arg Phe Ser Gly Gly Gly Gly
 50 55 60

Gly Gly Gly Val Gly Gly Ser Pro Ala His Ser Thr Ser Ala Ala Ser
 65 70 75 80

Gln Ser Gln Ser Gln Ser Gln Val Tyr Gly Arg Asp Ser Ser Leu Phe
 85 90 95

Gln Pro Phe Asn Val Pro Ser Asn Arg Pro Gly His Ser Thr Glu Lys
 100 105 110

Ile Asn Ser Asp Lys Ile Asn Lys Lys Ile Ser Gly Ser Arg Lys Glu
 115 120 125

Leu Gly Met Leu Ser Ser Gln Thr Lys Gly Met Asp Ile Tyr Ala Ser
 130 135 140

Arg Ser Thr Ala Glu Ala Pro Gln Arg Arg Ala Glu Asn Thr Ile Lys
 145 150 155 160

Ser Ser Ser Gly Lys Arg Leu Ala Asp Asp Asp Glu Phe Met Val Pro
 165 170 175

Ser Val Phe Asn Ser Arg Phe Pro Gln Tyr Ser Thr Gln Glu Asn Ala
 180 185 190

Gly Val Gln Asp Gln Ser Thr Pro Leu Val Ala Ala Asn Pro His Lys

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Ser	Pro	Ser	Thr	Val	Ser	Lys	Ser	Ser	Thr	Lys	Cys	Tyr	Asn	Thr	Val
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Ser	Lys	Lys	Leu	Glu	Arg	Ile	His	Val	Ser	Asp	Val	Lys	Ser	Arg	Thr
	225					230					235				240
Pro	Leu	Lys	Asp	Lys	Glu	Met	Glu	Ala	Ala	Gln	Thr	Ser	Lys	Asn	Val
				245					250					255	
Glu	Val	Glu	Lys	Ser	Ser	Ser	Phe	His	Ala	Ser	Lys	Asp	Met	Phe	Glu
			260					265					270		
Ser	Arg	His	Ala	Lys	Val	Tyr	Pro	Lys	Met	Asp	Lys	Thr	Gly	Ile	Ile
		275					280					285			
Asn	Asp	Ser	Asp	Glu	Pro	His	Gly	Gly	Asn	Ser	Gly	His	Gln	Ala	Thr
	290					295					300				
Ser	Arg	Asn	Gly	Gly	Ser	Met	Lys	Phe	Gln	Asn	Pro	Pro	Met	Arg	Arg
	305					310					315				320
Asn	Glu	Ile	Ser	Ser	Asn	Pro	Ser	Ser	Glu	Asn	Thr	Asp	Arg	His	Tyr
				325					330					335	
Asn	Leu	Pro	Gln	Gly	Gly	Ile	Glu	Glu	Thr	Gly	Thr	Lys	Arg	Lys	Arg
			340					345					350		
Leu	Leu	Glu	Gln	His	Asp	Ala	Glu	Lys	Ser	Asp	Asp	Val	Ser	Arg	Leu
		355					360					365			
Leu	Glu	Gln	His	Asp	Ala	Glu	Asn	Ile	Asp	Asp	Val	Ser	Asp	Ser	Ser
	370					375					380				
Val	Glu	Cys	Ile	Thr	Gly	Trp	Glu	Ile	Ser	Pro	Asp	Lys	Ile	Val	Gly
	385					390					395				400
Ala	Ile	Gly	Thr	Lys	His	Phe	Trp	Lys	Ala	Arg	Arg	Ala	Ile	Met	Asn
				405					410					415	
Gln	Gln	Arg	Val	Phe	Ala	Val	Gln	Val	Phe	Glu	Leu	His	Lys	Leu	Val
			420					425					430		

Lys Val Gln Lys Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Ser
435 440 445

Asp Pro Cys Leu Gly Asn Ala Leu Leu Gly Ser Lys Asn Lys Leu Val
450 455 460

Glu Glu Asn Leu Lys Ala Gln Pro Leu Leu Val Ala Thr Ile Asp Asp
465 470 475 480

Val Glu Pro Ser Leu Gln Gln Pro Glu Val Ser Lys Glu Asn Thr Glu
485 490 495

Asp Ser Pro Pro Ser Pro His Asp Thr Gly Leu Gly Ser Gly Gln Arg
500 505 510

Asp Gln Ala Ala Thr Asn Gly Val Ser Lys Ser Asn Arg Arg Ala Thr
515 520 525

Pro Val Ala Ser Asp Asn Lys Gln Asn Asn Trp Gly Val Gln Leu Gln
530 535 540

Pro Pro Gln Asn Gln Trp Leu Val Pro Val Met Ser Pro Leu Glu Gly
545 550 555 560

Leu Val Tyr Lys Pro Tyr Ser Gly Pro Cys Pro Pro Ala Gly Ser Ile
565 570 575

Leu Ala Pro Phe Tyr Ala Asn Cys Thr Pro Leu Ser Leu Pro Ser Thr
580 585 590

Ala Gly Asp Phe Met Asn Ser Ala Tyr Gly Val Pro Met Pro His Gln
595 600 605

Pro Gln His Met Gly Ala Pro Gly Pro Pro Ser Met Pro Met Asn Tyr
610 615 620

Phe Pro Pro Phe Ser Ile Pro Val Met Asn Pro Thr Ala Pro Ala Pro
625 630 635 640

Val Val Glu Gln Gly Arg His Pro Ser Met Pro Gln Pro Tyr Gly Asn
645 650 655

Phe Glu Gln Gln Ser Trp Ile Ser Cys Asn Met Ser His Pro Ser Gly
660 665 670

Ile Trp Arg Phe His Ala Ser Arg Asp Ser Glu Ala Gln Ala Ser Ser
675 680 685 .

Ala Ser Ser Pro Phe Asp Arg Phe Gln Cys Ser Gly Ser Gly Pro Val
690 695 700

Ser Ala Phe Pro Thr Val Ser Ala Gln Asn Asn Gln Pro Gln Pro Ser
705 710 715 720

Tyr Ser Ser Arg Asp Asn Gln Thr Asn Val Ile Lys Val Val Pro His
725 730 735

Asn Ser Arg Thr Ala Ser Glu Ser Ala Ala Arg Ile Phe Arg Ser Ile
740 745 750

Gln Met Glu Arg Gln Arg Asp Asp
755 760

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<213> Zea mays

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gctattgtca atcagcagag ggtatttgct gttcaagtat tcgagctgca taggttgatc 180
aaagtgcaga agttgatcgc tgcattctcca catgtactta ttgaggggga tccttgccctt 240
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cccgtttgaa ggacttgtct acaagcctta tcccgggsca ytgccctccg gtggaagtct 360
tttggcgccc ccattttttg ccagctaccc cacctcttcc tcctccacag ctggggggga 420
tttcatgagt tcggcatgtg gagccaggct gatgagtgcc cctgtgtact tcccgtcttt 480
cagcatgcct gcagtgtcag ggtctgcagt tgagcaagtg agccatgttg cagcgtcgca 540
gcataaacgg aactcgtgta gtgaagcggg gttggcatca agggacagcg aggtgcaagg 600
cagtagtgct agcagtcagg catcttctga aacagcagct caaccagggt tcattagggt 660

tgttccccac acggcacgca cggcttcaga gtcggcagca aggattttcc gctcaataca 720
 gatggagagg aaacaaaacg acccgtgact ggcagataaa aatgaaagaa cggagggagt 780
 agactaattt ttgaccgat aattataatg atcgccgtaa attggctggc ccgcccgcct 840
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Pro Gly Met Glu Ile Ser Pro Asp Asp Val Val Ser Ala Ile Gly Pro
 20 25 30

Lys His Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln Arg Val
 35 40 45

Phe Ala Val Gln Val Phe Glu Leu His Arg Leu Ile Lys Val Gln Lys
 50 55 60

Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Gly Asp Pro Cys Leu
65 70 75 80

Gly Lys Ser Leu Ala Val Ser Xaa Lys Arg Leu Ser Gln Trp Leu Ile
85 90 95

Pro Xaa Met Ser Pro Phe Glu Gly Leu Val Tyr Lys Pro Tyr Pro Gly
100 105 110

Xaa Xaa Pro Ser Gly Gly Ser Leu Leu Ala Pro Pro Phe Phe Ala Ser
115 120 125

Tyr Pro Thr Ser Ser Ser Ser Thr Ala Gly Gly Asp Phe Met Ser Ser
130 135 140

Ala Cys Gly Ala Arg Leu Met Ser Ala Pro Val Tyr Phe Pro Ser Phe
145 150 155 160

Ser Met Pro Ala Val Ser Gly Ser Ala Val Glu Gln Val Ser His Val
165 170 175

Ala Ala Ser Gln His Lys Arg Asn Ser Cys Ser Glu Ala Val Leu Ala
180 185 190

Ser Arg Asp Ser Glu Val Gln Gly Ser Ser Ala Ser Ser Pro Ala Ser
195 200 205

Ser Glu Thr Ala Ala Gln Pro Arg Val Ile Arg Val Val Pro His Thr
210 215 220

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225 230 235 240

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1				5				10						15		

tac	ttc	ccg	cct	ttc	agt	atg	cca	gtg	atg	aat	cca	gga	aca	cca	gca	96
Tyr	Phe	Pro	Pro	Phe	Ser	Met	Pro	Val	Met	Asn	Pro	Gly	Thr	Pro	Ala	
			20					25					30			

tct	gca	gtg	gag	caa	ggg	agc	cat	gct	gct	gcg	cca	cag	cct	cat	ggg	144
Ser	Ala	Val	Glu	Gln	Gly	Ser	His	Ala	Ala	Ala	Pro	Gln	Pro	His	Gly	
		35					40					45				

cac	atg	gac	cag	cag	tcg	ctg	atc	tca	tgt	aac	atg	tca	cac	ccg	agt	192
His	Met	Asp	Gln	Gln	Ser	Leu	Ile	Ser	Cys	Asn	Met	Ser	His	Pro	Ser	
	50					55					60					

ggc	gtt	tgg	agg	ttt	ctt	gca	tca	agg	gac	agc	gag	cca	cag	gcc	agc	240
Gly	Val	Trp	Arg	Phe	Leu	Ala	Ser	Arg	Asp	Ser	Glu	Pro	Gln	Ala	Ser	
65					70					75					80	

agc	gcc	acc	agc	cct	ttc	gac	agg	ctc	caa	gtc	caa	ggt	gat	gga	agt	288
Ser	Ala	Thr	Ser	Pro	Phe	Asp	Arg	Leu	Gln	Val	Gln	Gly	Asp	Gly	Ser	
				85					90					95		

gct	ccg	ttg	tca	ttc	ttt	ccc	acg	gct	tca	gct	ccg	aat	gtc	cag	cct	336
Ala	Pro	Leu	Ser	Phe	Phe	Pro	Thr	Ala	Ser	Ala	Pro	Asn	Val	Gln	Pro	
			100					105					110			

ccg	ccc	tca	tct	gga	ggc	cgg	gac	cgg	gac	cag	cag	aac	cat	gta	atc	384
Pro	Pro	Ser	Ser	Gly	Gly	Arg	Asp	Arg	Asp	Gln	Gln	Asn	His	Val	Ile	
		115					120					125				

agg	gtt	gtt	ccg	cgt	aac	gca	cag	act	gct	tca	gtc	ccg	aaa	gcc	caa	432
Arg	Val	Val	Pro	Arg	Asn	Ala	Gln	Thr	Ala	Ser	Val	Pro	Lys	Ala	Gln	
	130					135					140					

cct	cag	ccg	tca	tcc	gga	ggc	cgg	gac	caa	aag	aac	cat	gta	atc	agg	480
Pro	Gln	Pro	Ser	Ser	Gly	Gly	Arg	Asp	Gln	Lys	Asn	His	Val	Ile	Arg	
145					150					155					160	

gtt	gtt	ccg	cat	aac	gcg	cag	act	gct	tcg	gag	tca	gca	gcg	tgg	atc	528
Val	Val	Pro	His	Asn	Ala	Gln	Thr	Ala	Ser	Glu	Ser	Ala	Ala	Trp	Ile	
				165				170						175		

ttc	cgg	tca	ata	caa	atg	gag	agg	aac	caa	aat	gat	tcg	tag			570
Phe	Arg	Ser	Ile	Gln	Met	Glu	Arg	Asn	Gln	Asn	Asp	Ser				
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625

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 <213> Zea mays

<400> 31

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Tyr Phe Pro Pro Phe Ser Met Pro Val Met Asn Pro Gly Thr Pro Ala
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Ser Ala Val Glu Gln Gly Ser His Ala Ala Ala Pro Gln Pro His Gly
 35 40 45

His Met Asp Gln Gln Ser Leu Ile Ser Cys Asn Met Ser His Pro Ser
 50 55 60

Gly Val Trp Arg Phe Leu Ala Ser Arg Asp Ser Glu Pro Gln Ala Ser
 65 70 75 80

Ser Ala Thr Ser Pro Phe Asp Arg Leu Gln Val Gln Gly Asp Gly Ser
 85 90 95

Ala Pro Leu Ser Phe Phe Pro Thr Ala Ser Ala Pro Asn Val Gln Pro
 100 105 110

Pro Pro Ser Ser Gly Gly Arg Asp Arg Asp Gln Gln Asn His Val Ile
 115 120 125

Arg Val Val Pro Arg Asn Ala Gln Thr Ala Ser Val Pro Lys Ala Gln
 130 135 140

Pro Gln Pro Ser Ser Gly Gly Arg Asp Gln Lys Asn His Val Ile Arg
 145 150 155 160

Val Val Pro His Asn Ala Gln Thr Ala Ser Glu Ser Ala Ala Trp Ile
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Phe Arg Ser Ile Gln Met Glu Arg Asn Gln Asn Asp Ser
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 cttgaagcaa ccagacatga ccgcagagtc acacacacac acaccctaa gctttttgtc 180
 gtccccctcgt atggaatcca ttgtgggacg acacaaaaat atcttctttt gcttctctgc 240
 tttcttcttc ttcttcttaa aatttggttc tttcaggtgg atttgatctc catctacgta 300
 aaacaaaaac aaagtttata atctttttgg attttgggat tgatctaaag tgagatttgc 360
 atcttggcac taggttttgc aaggttacct aacaatttct ggttctgatt tcatttcttt 420
 aggttacgtg taagggaagg aattgttaat agggtttgtt tgtgagcgta gggaaaag 478
 atg gga gga atg aaa gat gaa gca aag agg ata aca att cct cca ttg 526
 Met Gly Gly Met Lys Asp Glu Ala Lys Arg Ile Thr Ile Pro Pro Leu
 1 5 10 15
 ttt cca agg gtt cat gtc aat gat act gga aga gga ggc ctg tct caa 574
 Phe Pro Arg Val His Val Asn Asp Thr Gly Arg Gly Gly Leu Ser Gln
 20 25 30
 caa ttt gat ggc aaa aca atg tct ctc gtc tct tct aaa cgt ccc aat 622
 Gln Phe Asp Gly Lys Thr Met Ser Leu Val Ser Ser Lys Arg Pro Asn
 35 40 45
 ctt cct tct ccg acc aac aac ata tct gat tct ctt tcc act ttc tct 670
 Leu Pro Ser Pro Thr Asn Asn Ile Ser Asp Ser Leu Ser Thr Phe Ser
 50 55 60
 ttg tct ctt cct cca cca cca aac aat gcc cgt ctc gtgagtcctt 716
 Leu Ser Leu Pro Pro Pro Pro Asn Asn Ala Arg Leu
 65 70 75
 ttaattcaact cattcaactt tcttggtttt gtgtgtctgc agatttatat acaagaatgg 776
 tgacaatgca tatttagatt atcactttat gacttggtga atactttttt gtaacag 833
 att gat gga cct gaa aag aat cag ttt tca cca atc tac aac aca aag 881
 Ile Asp Gly Pro Glu Lys Asn Gln Phe Ser Pro Ile Tyr Asn Thr Lys
 80 85 90
 ttt gag ggg aag ctg aat aaa aaa ggc ata aat tat aca agt cct aaa 929
 Phe Glu Gly Lys Leu Asn Lys Lys Gly Ile Asn Tyr Thr Ser Pro Lys
 95 100 105
 gga tca tca gtt act aat act aag cct agt tca ata aaa caa aat gag 977
 Gly Ser Ser Val Thr Asn Thr Lys Pro Ser Ser Ile Lys Gln Asn Glu
 110 115 120

tac ctc aag aac ctt acc agc ttg gat tct att aag tct cct att gtt Tyr Leu Lys Asn Leu Thr Ser Leu Asp Ser Ile Lys Ser Pro Ile Val 125 130 135 140	1025
ata cac tca gaa ata gat cca caa gca aac aca gat ttg tca ctc caa Ile His Ser Glu Ile Asp Pro Gln Ala Asn Thr Asp Leu Ser Leu Gln 145 150 155	1073
ttt tgt act agc ggt agc agt aaa ccc gga gga gag gct gtt gtt ggt Phe Cys Thr Ser Gly Ser Ser Lys Pro Gly Gly Glu Ala Val Val Gly 160 165 170	1121
tct aag atc ctt ttg tca gaa cgt ttg gaa gat gaa aac cag aat ggg Ser Lys Ile Leu Leu Ser Glu Arg Leu Glu Asp Glu Asn Gln Asn Gly 175 180 185	1169
tct ccc aat gtg atg aaa act caa tca tat aga aga aac ttt gct gag Ser Pro Asn Val Met Lys Thr Gln Ser Tyr Arg Arg Asn Phe Ala Glu 190 195 200	1217
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caa gtt gct tca aac tgc tct gca ata gag tct ttg tct ggt ata agt Gln Val Ala Ser Asn Cys Ser Ala Ile Glu Ser Leu Ser Gly Ile Ser 225 230 235	1313
gca tct tct tat gat att gcc aga gtg att ggt gaa aag agg ttt tgg Ala Ser Ser Tyr Asp Ile Ala Arg Val Ile Gly Glu Lys Arg Phe Trp 240 245 250	1361
aag atg aga aca tat atg atc aa gtttgtatcc tcctctcact tttcttatga Lys Met Arg Thr Tyr Met Ile Asn 255	1414
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atg gtaagctttt aataacctta ttgtttctgg tttgctttct atgcttcaga Met	1573
ttacttaata tgatgcag gtt caa aag atg gtt gcg aag tcg cca aac ttg Val Gln Lys Met Val Ala Lys Ser Pro Asn Leu 280 285	1624
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tca cat cag ctt gca atg gcg gct tca aag gtt aga aag cca aac act Ser His Gln Leu Ala Met Ala Ala Ser Lys Val Arg Lys Pro Asn Thr 305 310 315 320	1720

gag aat cac aaa cct gta cct gaa gaa tat cca gag cat atg aaa cca	1768
Glu Asn His Lys Pro Val Pro Glu Glu Tyr Pro Glu His Met Lys Pro	
325 330 335	
aag ctt cct cta cct tcc ata agc aaa gaa ctc gtg act cct att tgg	1816
Lys Leu Pro Leu Pro Ser Ile Ser Lys Glu Leu Val Thr Pro Ile Trp	
340 345 350	
cca caa cag cta ctt cct cct cct gga aac caa tgg tta gtt cct gta	1864
Pro Gln Gln Leu Leu Pro Pro Pro Gly Asn Gln Trp Leu Val Pro Val	
355 360 365	
ata act gat tca gac ggt ctg gtc tat aaa cca ttt cca gga cca tgt	1912
Ile Thr Asp Ser Asp Gly Leu Val Tyr Lys Pro Phe Pro Gly Pro Cys	
370 375 380	
cct cct tct tct tca gcc ttc atg gtt cca gtt tat ggc caa gat tca	1960
Pro Pro Ser Ser Ser Ala Phe Met Val Pro Val Tyr Gly Gln Asp Ser	
385 390 395 400	
ctc gag aca cca ttc agg ttc cct gtt tct tct cca ttc agc cac agc	2008
Leu Glu Thr Pro Phe Arg Phe Pro Val Ser Ser Pro Phe Ser His Ser	
405 410 415	
tac ttc cca cct cct aac gcg agg aca aca gtt gac caa aca aac ccg	2056
Tyr Phe Pro Pro Pro Asn Ala Arg Thr Thr Val Asp Gln Thr Asn Pro	
420 425 430	
ttt ggt cag ttt caa aga tgg tct aac aca tca agc cac atg aca caa	2104
Phe Gly Gln Phe Gln Arg Trp Ser Asn Thr Ser Ser His Met Thr Gln	
435 440 445	
gcc att cca ttt tct tta aag aag tct cag gaa tct aat gac agt gac	2152
Ala Ile Pro Phe Ser Leu Lys Lys Ser Gln Glu Ser Asn Asp Ser Asp	
450 455 460	
ata cat gga agc aca gct tca agt cca cca gag aag cat aaa ctt gaa	2200
Ile His Gly Ser Thr Ala Ser Ser Pro Pro Glu Lys His Lys Leu Glu	
465 470 475 480	
gtg ctt cct ctg ttt cct aca gag cct acc cat caa act gat gag tac	2248
Val Leu Pro Leu Phe Pro Thr Glu Pro Thr His Gln Thr Asp Glu Tyr	
485 490 495	
aag cag aaa cag caa ccg atg ctt cgc gcc att aaa gcc gtt cct cat	2296
Lys Gln Lys Gln Gln Pro Met Leu Arg Ala Ile Lys Ala Val Pro His	
500 505 510	
aat tca aca tct gcc tct gaa tct gct gca agg atc ttc cgt ttc att	2344
Asn Ser Thr Ser Ala Ser Glu Ser Ala Ala Arg Ile Phe Arg Phe Ile	
515 520 525	
cag gaa gaa agg agg gac tca gat cat atg att agt tag ttcttttata	2393
Gln Glu Glu Arg Arg Asp Ser Asp His Met Ile Ser	
530 535 540	

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 atacacacac ttatacacac atcttacatt gttcttgtat tgacaaacag ctaataaaag 2573
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<400> 33

Met Gly Gly Met Lys Asp Glu Ala Lys Arg Ile Thr Ile Pro Pro Leu
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Gln Phe Asp Gly Lys Thr Met Ser Leu Val Ser Ser Lys Arg Pro Asn
 35 40 45

Leu Pro Ser Pro Thr Asn Asn Ile Ser Asp Ser Leu Ser Thr Phe Ser
 50 55 60

Leu Ser Leu Pro Pro Pro Pro Asn Asn Ala Arg Leu Ile Asp Gly Pro
 65 70 75 80

Glu Lys Asn Gln Phe Ser Pro Ile Tyr Asn Thr Lys Phe Glu Gly Lys
 85 90 95

Leu Asn Lys Lys Gly Ile Asn Tyr Thr Ser Pro Lys Gly Ser Ser Val
 100 105 110

Thr Asn Thr Lys Pro Ser Ser Ile Lys Gln Asn Glu Tyr Leu Lys Asn
 115 120 125

Leu Thr Ser Leu Asp Ser Ile Lys Ser Pro Ile Val Ile His Ser Glu
 130 135 140

Ile Asp Pro Gln Ala Asn Thr Asp Leu Ser Leu Gln Phe Cys Thr Ser
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Asp Ile Ala Arg Val Ile Gly Glu Lys Arg Phe Trp Lys Met Arg Thr
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Tyr Met Ile Asn Gln Gln Lys Ile Phe Ala Gly Gln Val Phe Glu Leu
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Ile His Gly Ser Thr Ala Ser Ser Pro Pro Glu Lys His Lys Leu Glu
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Val Leu Pro Leu Phe Pro Thr Glu Pro Thr His Gln Thr Asp Glu Tyr
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Lys Leu Ile Ala Ala Ser Pro Asp Leu Leu Leu Asp Glu Ile Ser Phe	
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Leu Gly Lys Val Ser Ala Lys Ser Tyr Pro Val Lys Lys Leu Leu Pro	
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Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Ile Tyr Lys Pro	
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His Pro Gly Met Ala His Thr Gly His Tyr Gly Gly Tyr Tyr Gly His	
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Tyr Met Pro Thr Pro Met Val Met Pro Gln Tyr His Pro Gly Met Gly	
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Thr Ile Met Asn Pro Tyr Cys Ser Ser Gln Gln Gln Gln Gln Gln Gln	
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Gly Ser Thr Gly Ser Ser Pro Ser Gly Pro Gln Gly Ile Ser Gly Ser	
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Lys Ser Phe Arg Pro Phe Ala Ala Val Asp Glu Asp Ser Asn Ile Asn	
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Phe Gly Asp His Gly Thr Met Asn Ser Arg Ser Asn Asn Thr Ser Thr
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Leu Val His Pro Gly Pro Ser Ser Gln Pro Cys Gly Val Glu Arg Asn
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Leu Ser Val Gln His Leu Asp Ser Ser Ala Ala Asn Gln Ala Thr Glu
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Lys Phe Val Ser Gln Met Ser Phe Met Glu Asn Val Arg Ser Ser Ala
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Gln His Asp Gln Arg Lys Met Val Arg Glu Glu Glu Asp Phe Ala Val
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Pro Val Tyr Ile Asn Ser Arg Arg Ser Gln Ser His Gly Arg Thr Lys
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Ser Gly Ile Glu Lys Glu Lys His Thr Pro Met Val Ala Pro Ser Ser
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His His Ser Ile Arg Phe Gln Glu Val Asn Gln Thr Gly Ser Lys Gln
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Val Thr Glu Glu Ile Asp Leu Glu Lys Ser Ala Ser Ser His Asp Arg
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Val Asn Asp Tyr Asn Ala Ser Leu Arg Gln Glu Ser Arg Asn Arg Leu
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Tyr Arg Asp Gly Gly Lys Thr Arg Leu Lys Asp Thr Asp Asn Gly Ala
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Pro Glu Asp Ile Asp Asn Asp Arg Glu Tyr Ser Lys Ser Arg Ala Cys
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370 375 380

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Gly Leu Ile Tyr Lys Pro His Pro Gly Met Ala His Thr Gly His Tyr
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Gly Gly Tyr Tyr Gly His Tyr Met Pro Thr Pro Met Val Met Pro Gln
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Tyr His Pro Gly Met Gly Phe Pro Pro Pro Gly Asn Gly Tyr Phe Pro
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Glu Pro Ala Pro Gln Gln Gln Gln Gln Pro Thr Lys Ser Tyr Pro Arg

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Glu Asp Ser Asn Ile Asn Asn Ala Pro Glu Gln Thr Met Thr Thr Thr		
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Thr Thr Thr Thr Arg Thr Thr Val Thr Gln Thr Thr Arg Asp Gly Gly		
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Gly Val Thr Arg Val Ile Lys Val Val Pro His Asn Ala Lys Leu Ala		
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ang ggg ccg tta ttn cct agg tta cat gtt ggt gat aca gag aag gga      460
Xaa Gly Pro Leu Xaa Pro Arg Leu His Val Gly Asp Thr Glu Lys Gly
                        15          20          25
ggg cca aga gca cct cct agg aat aaa ttg gct ctc tat gag caa ttt      508
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 Ala Ala Arg Ile Phe Gln Ser Ile Gln Glu Glu Arg Lys Gln Tyr Asp
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Val Gln His Leu Ile

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gct gaa tca tca aat ctt ttg ccc gat act gct gct gtt ttg gga aaa 155

Ala Glu Ser Ser Asn Leu Leu Pro Asp Thr Ala Ala Val Leu Gly Lys

10 15 20 25

cct ctt ctg cag gga tct aat tct aaa agc ctt tca ttt gaa gaa gtt 203

Pro Leu Leu Gln Gly Ser Asn Ser Lys Ser Leu Ser Phe Glu Glu Val

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ggt gaa cct cag gca caa aat cat aaa cag caa gac cat tct gaa aac 251

Val	Glu	Pro	Gln	Ala	Gln	Asn	His	Lys	Gln	Gln	Asp	His	Ser	Glu	Asn		
			45					50					55				
caa	aac	cat	aaa	ttg	gat	tat	tct	act	gaa	aat	gga	gtt	ggg	aaa	aca		299
Gln	Asn	His	Lys	Leu	Asp	Tyr	Ser	Thr	Glu	Asn	Gly	Val	Gly	Lys	Thr		
		60					65					70					
tcc	tta	tca	tcc	caa	aaa	tca	aac	cag	gca	aat	gct	ggg	tca	cag	tgt		347
Ser	Leu	Ser	Ser	Gln	Lys	Ser	Asn	Gln	Ala	Asn	Ala	Gly	Ser	Gln	Cys		
	75					80					85						
ttt	aat	caa	tca	cct	gga	cat											368
Phe	Asn	Gln	Ser	Pro	Gly	His											
90					95												

<210> 41
 <211> 96
 <212> PRT
 <213> Pisum sativum

<400> 41

Arg	Leu	Ile	Lys	Val	Gln	His	Leu	Ile	Ala	Glu	Ser	Ser	Asn	Leu	Leu		
1			5						10					15			
Pro	Asp	Thr	Ala	Ala	Val	Leu	Gly	Lys	Pro	Leu	Leu	Gln	Gly	Ser	Asn		
			20					25					30				
Ser	Lys	Ser	Leu	Ser	Phe	Glu	Glu	Val	Val	Glu	Pro	Gln	Ala	Gln	Asn		
		35					40					45					
His	Lys	Gln	Gln	Asp	His	Ser	Glu	Asn	Gln	Asn	His	Lys	Leu	Asp	Tyr		
	50					55					60						
Ser	Thr	Glu	Asn	Gly	Val	Gly	Lys	Thr	Ser	Leu	Ser	Ser	Gln	Lys	Ser		
65					70					75				80			
Asn	Gln	Ala	Asn	Ala	Gly	Ser	Gln	Cys	Phe	Asn	Gln	Ser	Pro	Gly	His		
			85						90					95			

<210> 42
 <211> 523
 <212> DNA
 <213> Pisum sativum

<220>
 <221> exon
 <222> (2)..(523)
 <223> Partial

<400> 42
a tat ccc ggg cct gga ttt aca gga aca aat ttt gga gga tgt ggg ccc 49
Tyr Pro Gly Pro Gly Phe Thr Gly Thr Asn Phe Gly Gly Cys Gly Pro
1 5 10 15

tac gcg gct gct cct tcg ggt ggc act ttt atg aat cct tcc tat gga 97
Tyr Ala Ala Ala Pro Ser Gly Gly Thr Phe Met Asn Pro Ser Tyr Gly
20 25 30

atc ccg cct cca cca gag act cct cca ggc agt caa gct tac ttc cct 145
Ile Pro Pro Pro Glu Thr Pro Pro Gly Ser Gln Ala Tyr Phe Pro
35 40 45

ccc tac ggt ggc atg cca gtt atg aaa gct gca gct tca gag tca gct 193
Pro Tyr Gly Gly Met Pro Val Met Lys Ala Ala Ala Ser Glu Ser Ala
50 55 60

gtt gaa cat gtg aac caa ttc tcc gca cgc ggg caa agt cgt cgt tta 241
Val Glu His Val Asn Gln Phe Ser Ala Arg Gly Gln Ser Arg Arg Leu
65 70 75 80

tct gaa gat gaa gct gat tgt aac aaa cac aat caa agc tca tac gat 289
Ser Glu Asp Glu Ala Asp Cys Asn Lys His Asn Gln Ser Ser Tyr Asp
85 90 95

tta cca gtt cag aga aat gga gct aca tca cat gtc atg tat cat cag 337
Leu Pro Val Gln Arg Asn Gly Ala Thr Ser His Val Met Tyr His Gln
100 105 110

aga tcc aag gag ttt gag gtg cag atg agt aca gca agt agt cct agc 385
Arg Ser Lys Glu Phe Glu Val Gln Met Ser Thr Ala Ser Ser Pro Ser
115 120 125

gaa atg gca caa gaa atg agc acg gga caa gtt gcc gaa ggg aga gat 433
Glu Met Ala Gln Glu Met Ser Thr Gly Gln Val Ala Glu Gly Arg Asp
130 135 140

gta cta cct ctt ttc cct atg gtt cca gta gaa cca gag agt gta cct 481
Val Leu Pro Leu Phe Pro Met Val Pro Val Glu Pro Glu Ser Val Pro
145 150 155 160

cat tct ctc gaa aca gga caa aaa act cga gtt atc aaa gtg 523
His Ser Leu Glu Thr Gly Gln Lys Thr Arg Val Ile Lys Val
165 170

<210> 43
<211> 174
<212> PRT
<213> Pisum sativum

<400> 43
Tyr Pro Gly Pro Gly Phe Thr Gly Thr Asn Phe Gly Gly Cys Gly Pro
1 5 10 15

Tyr Ala Ala Ala Pro Ser Gly Gly Thr Phe Met Asn Pro Ser Tyr Gly
 20 25 30

Ile Pro Pro Pro Pro Glu Thr Pro Pro Gly Ser Gln Ala Tyr Phe Pro
 35 40 45

Pro Tyr Gly Gly Met Pro Val Met Lys Ala Ala Ala Ser Glu Ser Ala
 50 55 60

Val Glu His Val Asn Gln Phe Ser Ala Arg Gly Gln Ser Arg Arg Leu
 65 70 75 80

Ser Glu Asp Glu Ala Asp Cys Asn Lys His Asn Gln Ser Ser Tyr Asp
 85 90 95

Leu Pro Val Gln Arg Asn Gly Ala Thr Ser His Val Met Tyr His Gln
 100 105 110

Arg Ser Lys Glu Phe Glu Val Gln Met Ser Thr Ala Ser Ser Pro Ser
 115 120 125

Glu Met Ala Gln Glu Met Ser Thr Gly Gln Val Ala Glu Gly Arg Asp
 130 135 140

Val Leu Pro Leu Phe Pro Met Val Pro Val Glu Pro Glu Ser Val Pro
 145 150 155 160

His Ser Leu Glu Thr Gly Gln Lys Thr Arg Val Ile Lys Val
 165 170

<210> 44
 <211> 395
 <212> DNA
 <213> Glycine max

<220>
 <221> Intron
 <222> (1)..(301)
 <223> partial

<220>
 <221> exon
 <222> (302)..(395)
 <223> partial

<400> 44
 ttatgtcttg ttaatatgtc gagtcctcct gaaaaaacca tgttaagatt tgtatgatga 60
 tatgatataa attgtagaac ggaagatatt ccgcttaact gctaaccggt tttgtgatgt 120
 gatcggagcc tctgattttg gtagttagtg gtttatatat cggtgcttcc atgttccaac 180
 atgattatag atagctccaa acgcttaata tttccctttt atttcaactg tatatttctc 240
 aagtcctaata aggacgagta ttgtgcaatt ttcttgatcc aactcctggt cctctctaca 300
 g tca aca gag agt gtt tgc tgt cca agt gtt tga gtt gca tag act gat 349
 Ser Thr Glu Ser Val Cys Cys Pro Ser Val Val Ala Thr Asp
 1 5 10
 aaa ggt cca aca gct aat tgc tgg atc acc aga tat ttt gct tga a 395
 Lys Gly Pro Thr Ala Asn Cys Trp Ile Thr Arg Tyr Phe Ala
 15 20 25

<210> 45
 <211> 31
 <212> PRT
 <213> Glycine max

<400> 45
 Gln Gln Arg Val Phe Ala Val Gln Val Phe Glu Leu His Arg Leu Ile
 1 5 10 15
 Lys Val Gln Gln Leu Ile Ala Gly Ser Pro Asp Ile Leu Leu Glu
 20 25 30

<210> 46
 <211> 477
 <212> DNA
 <213> Xanthium

<220>
 <221> exon
 <222> (2)..(13)
 <223> partial

<220>
 <221> exon
 <222> (145)..(477)
 <223> partial

<220>
 <221> Intron
 <222> (14)..(144)
 <223> partial

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<400> 46
t cga cta ata rag gtaaagcaac tccaaaggct gaatctcttg tagcaatttg      53
  Arg Leu Ile Xaa
  1

gggggaggggt gtgaaataga aaatatgatac tatatactgt ttttcgattc attactacgc 113

tgctcatgca tttttcctgt tattttaaca g gtc cag aag ctc att gcc gag      165
                               Val Gln Lys Leu Ile Ala Glu
                               5                               10

tca cca aac agt atg ctt gaa gat gct gct tat tta ggc aaa cca tta      213
Ser Pro Asn Ser Met Leu Glu Asp Ala Ala Tyr Leu Gly Lys Pro Leu
          15                               20                               25

aag agt tcg tct ggt aaa aga ctg cca ttg gag tgt att att aga gaa      261
Lys Ser Ser Ser Gly Lys Arg Leu Pro Leu Glu Cys Ile Ile Arg Glu
          30                               35                               40

tct caa agt gtt ccg aag cgc aag aat gat tct gag aag cct aac ttc      309
Ser Gln Ser Val Pro Lys Arg Lys Asn Asp Ser Glu Lys Pro Asn Phe
          45                               50                               55

agg atg gaa tgc tct gct gaa aac act gtg ggg aag gca tct ctt tct      357
Arg Met Glu Cys Ser Ala Glu Asn Thr Val Gly Lys Ala Ser Leu Ser
          60                               65                               70                               75

tct gtg caa aac agt agc cag ctc tct agc cac aga cca ttt tca gga      405
Ser Val Gln Asn Ser Ser Gln Leu Ser Ser His Arg Pro Phe Ser Gly
          80                               85                               90

aat ccc cca cca acg cct gtg aca aac gat gct aac acg agt ccc tgg      453
Asn Pro Pro Pro Thr Pro Val Thr Asn Asp Ala Asn Thr Ser Pro Trp
          95                               100                               105

tgc ttt caa caa cct ccg ggg cac      477
Cys Phe Gln Gln Pro Pro Gly His
          110                               115

<210> 47
<211> 115
<212> PRT
<213> Xanthium

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa = uncertain amino acid residue

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<400> 47

Arg Leu Ile Xaa Val Gln Lys Leu Ile Ala Glu Ser Pro Asn Ser Met
1                               5                               10                               15

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Leu Glu Asp Ala Ala Tyr Leu Gly Lys Pro Leu Lys Ser Ser Ser Gly
 20 25 30

Lys Arg Leu Pro Leu Glu Cys Ile Ile Arg Glu Ser Gln Ser Val Pro
 35 40 45

Lys Arg Lys Asn Asp Ser Glu Lys Pro Asn Phe Arg Met Glu Cys Ser
 50 55 60

Ala Glu Asn Thr Val Gly Lys Ala Ser Leu Ser Ser Val Gln Asn Ser
 65 70 75 80

Ser Gln Leu Ser Ser His Arg Pro Phe Ser Gly Asn Pro Pro Pro Thr
 85 90 95

Pro Val Thr Asn Asp Ala Asn Thr Ser Pro Trp Cys Phe Gln Gln Pro
 100 105 110

Pro Gly His
 115

<210> 48
 <211> 433
 <212> DNA
 <213> Xanthium

<220>
 <221> exon
 <222> (2)..(13)
 <223> partial

<220>
 <221> exon
 <222> (128)..(433)
 <223> partial

<220>
 <221> Intron
 <222> (14)..(127)
 <223> partial

<400> 48
 t mga cta ctc rag gtaaagcaac tgtagagact gaataacttc aattatcagc
 Xaa Leu Leu Xaa
 1

53

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tttgagattt tgcattccct gtttttcctt ggacttggtta ttttgctcaa atttttctgt      113

ttgttactca ttag gtc cag aaa ctg ata gct agt tcg cca aat agt ata      163
                Val Gln Lys Leu Ile Ala Ser Ser Pro Asn Ser Ile
                5                10                15

ctc gaa gat ggt tct tct tta ggc aaa cct tta aag agg ttg tct act      211
Leu Glu Asp Gly Ser Ser Leu Gly Lys Pro Leu Lys Arg Leu Ser Thr
                20                25                30

aaa aga ctt gca ttg gag tat aat gtc aaa gca cct gaa aat gtt tcg      259
Lys Arg Leu Ala Leu Glu Tyr Asn Val Lys Ala Pro Glu Asn Val Ser
                35                40                45

aaa cag aag aat gat tct gag aag cct aac tct agg atg gaa tcc aat      307
Lys Gln Lys Asn Asp Ser Glu Lys Pro Asn Ser Arg Met Glu Ser Asn
                50                55                60

gcc gaa aat gat gta gga gag aca tct ctt tct tgc cgc aga cca ctt      355
Ala Glu Asn Asp Val Gly Glu Thr Ser Leu Ser Cys Arg Arg Pro Leu
65                70                75                80

tca gaa acc ccg tca cca aca cca gta aaa cac gtt tcc cac atg ggt      403
Ser Glu Thr Pro Ser Pro Thr Pro Val Lys His Val Ser His Met Gly
                85                90                95

ccg tgg ctc ttc aat caa cct tcg gga cac      433
Pro Trp Leu Phe Asn Gln Pro Ser Gly His
                100                105

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<210> 49
<211> 106
<212> PRT
<213> Xanthium

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<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa = uncertain amino acid residue

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<400> 49

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Arg Leu Leu Xaa Val Gln Lys Leu Ile Ala Ser Ser Pro Asn Ser Ile
1                5                10                15

Leu Glu Asp Gly Ser Ser Leu Gly Lys Pro Leu Lys Arg Leu Ser Thr
                20                25                30

Lys Arg Leu Ala Leu Glu Tyr Asn Val Lys Ala Pro Glu Asn Val Ser
35                40                45

```


Lys Gln Lys Asn Asp Ser Glu Lys Pro Asn Ser Arg Met Glu Ser Asn
 50 55 60

Ala Glu Asn Asp Val Gly Glu Thr Ser Leu Ser Cys Arg Arg Pro Leu
 65 70 75 80

Ser Glu Thr Pro Ser Pro Thr Pro Val Lys His Val Ser His Met Gly
 85 90 95

Pro Trp Leu Phe Asn Gln Pro Ser Gly His
 100 105

<210> 50
 <211> 526
 <212> DNA
 <213> Xanthium

<220>
 <221> exon
 <222> (2)..(526)
 <223> partial

<400> 50
 a cat cct gga cct gca ttc atg agt cca gta tat ggc ggt tgt gga ccc 49
 His Pro Gly Pro Ala Phe Met Ser Pro Val Tyr Gly Gly Cys Gly Pro
 1 5 10 15
 ccg att cca atg acg gga aac ttt tta gct ccg gca tac tat caa gga 97
 Pro Ile Pro Met Thr Gly Asn Phe Leu Ala Pro Ala Tyr Tyr Gln Gly
 20 25 30
 acg gga gct cct ttc gca cct caa cct agt cat ggc tac ttt cct ccg 145
 Thr Gly Ala Pro Phe Ala Pro Gln Pro Ser His Gly Tyr Phe Pro Pro
 35 40 45
 ttt gac atg cca gtt atg aat cca gta atc cca tct cca gct att gat 193
 Phe Asp Met Pro Val Met Asn Pro Val Ile Pro Ser Pro Ala Ile Asp
 50 55 60
 caa ccg gac cag gtt gct gca acg ggt ttt caa ggt ctg tta tcg aga 241
 Gln Pro Asp Gln Val Ala Ala Thr Gly Phe Gln Gly Leu Leu Ser Arg
 65 70 75 80
 gat cag gaa gtt aat ttt cac att caa caa cag aac tca agt aat gtt 289
 Asp Gln Glu Val Asn Phe His Ile Gln Gln Gln Asn Ser Ser Asn Val
 85 90 95
 gcg aga gag aat aat gta gcc gcg cca aag gtt gtg aga ttg tat ccc 337
 Ala Arg Glu Asn Asn Val Ala Ala Pro Lys Val Val Arg Leu Tyr Pro
 100 105 110
 tct aga gat tct gag ttg caa gcc agc act gca agt agt cca agg gaa 385

Ser Arg Asp Ser Glu Leu Gln Ala Ser Thr Ala Ser Ser Pro Arg Glu
 115 120 125
 aga ggt cat gga tta gac gtg ggc aac tcc acc gga gga aga agc gtg 433
 Arg Gly His Gly Leu Asp Val Gly Asn Ser Thr Gly Gly Arg Ser Val
 130 135 140
 ttt cct ctg ttc cca act ttt cct gct att agc aac ccc gct agt agc 481
 Phe Pro Leu Phe Pro Thr Phe Pro Ala Ile Ser Asn Pro Ala Ser Ser
 145 150 155 160
 tcc cag cct cat ttt cct agt cat acg gct aga gtt atc aaa gtt 526
 Ser Gln Pro His Phe Pro Ser His Thr Ala Arg Val Ile Lys Val
 165 170 175

 <210> 51
 <211> 175
 <212> PRT
 <213> Xanthium

 <400> 51

 His Pro Gly Pro Ala Phe Met Ser Pro Val Tyr Gly Gly Cys Gly Pro
 1 5 10 15

 Pro Ile Pro Met Thr Gly Asn Phe Leu Ala Pro Ala Tyr Tyr Gln Gly
 20 25 30

 Thr Gly Ala Pro Phe Ala Pro Gln Pro Ser His Gly Tyr Phe Pro Pro
 35 40 45

 Phe Asp Met Pro Val Met Asn Pro Val Ile Pro Ser Pro Ala Ile Asp
 50 55 60

 Gln Pro Asp Gln Val Ala Ala Thr Gly Phe Gln Gly Leu Leu Ser Arg
 65 70 75 80

 Asp Gln Glu Val Asn Phe His Ile Gln Gln Gln Asn Ser Ser Asn Val
 85 90 95

 Ala Arg Glu Asn Asn Val Ala Ala Pro Lys Val Val Arg Leu Tyr Pro
 100 105 110

 Ser Arg Asp Ser Glu Leu Gln Ala Ser Thr Ala Ser Ser Pro Arg Glu
 115 120 125

 Arg Gly His Gly Leu Asp Val Gly Asn Ser Thr Gly Gly Arg Ser Val
 130 135 140

Phe Pro Leu Phe Pro Thr Phe Pro Ala Ile Ser Asn Pro Ala Ser Ser
 145 150 155 160

Ser Gln Pro His Phe Pro Ser His Thr Ala Arg Val Ile Lys Val
 165 170 175

<210> 52
 <211> 532
 <212> DNA
 <213> poplar trees

<220>
 <221> exon
 <222> (2)..(532)
 <223> partial

<400> 52
 t tac act gcc cck gga ttc atg gga tcg ggt tgt gga gga tgt gga cct 49
 Tyr Thr Ala Xaa Gly Phe Met Gly Ser Gly Cys Gly Gly Cys Gly Pro
 1 5 10 15
 ttt ggg cca att ccc ttg aca gac aac ttt atg act tca gct tat gcg 97
 Phe Gly Pro Ile Pro Leu Thr Asp Asn Phe Met Thr Ser Ala Tyr Ala
 20 25 30
 att cca aca tct cat tat cat caa ggt att ggg gtc tca cca ggt gct 145
 Ile Pro Thr Ser His Tyr His Gln Gly Ile Gly Val Ser Pro Gly Ala
 35 40 45
 cct cca gtt ggt aat gct tgc ttc gcc cca tat ggc atg cca gga atg 193
 Pro Pro Val Gly Asn Ala Cys Phe Ala Pro Tyr Gly Met Pro Gly Met
 50 55 60
 aac cca gcc atc tca ggt tct gca ggg tct ggt tcc tgt ggt caa act 241
 Asn Pro Ala Ile Ser Gly Ser Ala Gly Ser Gly Ser Cys Gly Gln Thr
 65 70 75 80
 gct cag ttt cca gga ggc att ttg agc tcg aac atg cca cat caa agc 289
 Ala Gln Phe Pro Gly Gly Ile Leu Ser Ser Asn Met Pro His Gln Ser
 85 90 95
 tca tgt aat gaa cgg act caa aag agt gaa gct gtt tta gaa ggt atg 337
 Ser Cys Asn Glu Arg Thr Gln Lys Ser Glu Ala Val Leu Glu Gly Met
 100 105 110
 aag ctt cgg gca tct aaa aac act tcg gta caa gga agt aca ggt agt 385
 Lys Leu Arg Ala Ser Lys Asn Thr Ser Val Gln Gly Ser Thr Gly Ser
 115 120 125
 agt ccc agt ggc aga gtg caa ggg gtt ggg act gtt caa gcc gct gat 433
 Ser Pro Ser Gly Arg Val Gln Gly Val Gly Thr Val Gln Ala Ala Asp
 130 135 140

gga aga gct gcg ttc cca cct ttc cca gtg act cct cct tgc cct gag	481
Gly Arg Ala Ala Phe Pro Pro Phe Pro Val Thr Pro Pro Cys Pro Glu	
145 150 155 160	

gga gcc cct cag cat caa gag aca gac cag ctg tcg aaa gtg atc aag	529
Gly Ala Pro Gln His Gln Glu Thr Asp Gln Leu Ser Lys Val Ile Lys	
165 170 175	

gtt	532
Val	

<210> 53
 <211> 177
 <212> PRT
 <213> Poplar trees

 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> Xaa = uncertain amino acid residue

<400> 53

Tyr Thr Ala Xaa Gly Phe Met Gly Ser Gly Cys Gly Gly Cys Gly Pro
1 5 10 15

Phe Gly Pro Ile Pro Leu Thr Asp Asn Phe Met Thr Ser Ala Tyr Ala
20 25 30

Ile Pro Thr Ser His Tyr His Gln Gly Ile Gly Val Ser Pro Gly Ala
35 40 45

Pro Pro Val Gly Asn Ala Cys Phe Ala Pro Tyr Gly Met Pro Gly Met
50 55 60

Asn Pro Ala Ile Ser Gly Ser Ala Gly Ser Gly Ser Cys Gly Gln Thr
65 70 75 80

Ala Gln Phe Pro Gly Gly Ile Leu Ser Ser Asn Met Pro His Gln Ser
85 90 95

Ser Cys Asn Glu Arg Thr Gln Lys Ser Glu Ala Val Leu Glu Gly Met
100 105 110

Lys Leu Arg Ala Ser Lys Asn Thr Ser Val Gln Gly Ser Thr Gly Ser
115 120 125

Ser Pro Ser Gly Arg Val Gln Gly Val Gly Thr Val Gln Ala Ala Asp
 130 135 140

Gly Arg Ala Ala Phe Pro Pro Phe Pro Val Thr Pro Pro Cys Pro Glu
 145 150 155 160

Gly Ala Pro Gln His Gln Glu Thr Asp Gln Leu Ser Lys Val Ile Lys
 165 170 175

Val

<210> 54
 <211> 418
 <212> DNA
 <213> Mimulus sp.

<220>
 <221> exon
 <222> (2)..(418)
 <223>

<400> 54
 g tac ccg ttc gtc agc caa ccc tgt gga ggg ggc tgc ggc ccc cct gga 49
 Tyr Pro Phe Val Ser Gln Pro Cys Gly Gly Gly Cys Gly Pro Pro Gly
 1 5 10 15

tcg aat cca acg gtg gga aat ttc tca act cca cca ccg cca caa tat 97
 Ser Asn Pro Thr Val Gly Asn Phe Ser Thr Pro Pro Pro Pro Gln Tyr
 20 25 30

cat cat tta cct tct ttc cct cag ttc ccc ccc cac ggc tac ttc cct 145
 His His Leu Pro Ser Phe Pro Gln Phe Pro Pro His Gly Tyr Phe Pro
 35 40 45

cct tac tgt gtc ccg att atg gac acg tca gca ttc tcg ggc ccg ccc 193
 Pro Tyr Cys Val Pro Ile Met Asp Thr Ser Ala Phe Ser Gly Pro Pro
 50 55 60

ccc gaa cag acc ata cga gcc cca gct gct gca ggc cca gct gta caa 241
 Pro Glu Gln Thr Ile Arg Ala Pro Ala Ala Gly Pro Ala Val Gln
 65 70 75 80

aaa agc ggg ccc gct tta tgg gat gtc gaa atg caa ggg agc aca gct 289
 Lys Ser Gly Pro Ala Leu Trp Asp Val Glu Met Gln Gly Ser Thr Ala
 85 90 95

agt agc ccg agt ggg agg cgt aaa aga gga agc aac ggt gtt gaa ttt 337
 Ser Ser Pro Ser Gly Arg Arg Lys Arg Gly Ser Asn Gly Val Glu Phe
 100 105 110

gaa aga agg aat atg ctt ccg ctt ttc ccc act acc cca gct gct gtg 385
 Glu Arg Arg Asn Met Leu Pro Leu Phe Pro Thr Thr Pro Ala Ala Val
 115 120 125

gat gcc ttg aaa cca acg cgg gtg att aag gtt 418
 Asp Ala Leu Lys Pro Thr Arg Val Ile Lys Val
 130 135

<210> 55
 <211> 139
 <212> PRT
 <213> Mimulus sp.

<400> 55

Tyr Pro Phe Val Ser Gln Pro Cys Gly Gly Gly Cys Gly Pro Pro Gly
 1 5 10 15

Ser Asn Pro Thr Val Gly Asn Phe Ser Thr Pro Pro Pro Pro Gln Tyr
 20 25 30

His His Leu Pro Ser Phe Pro Gln Phe Pro Pro His Gly Tyr Phe Pro
 35 40 45

Pro Tyr Cys Val Pro Ile Met Asp Thr Ser Ala Phe Ser Gly Pro Pro
 50 55 60

Pro Glu Gln Thr Ile Arg Ala Pro Ala Ala Ala Gly Pro Ala Val Gln
 65 70 75 80

Lys Ser Gly Pro Ala Leu Trp Asp Val Glu Met Gln Gly Ser Thr Ala
 85 90 95

Ser Ser Pro Ser Gly Arg Arg Lys Arg Gly Ser Asn Gly Val Glu Phe
 100 105 110

Glu Arg Arg Asn Met Leu Pro Leu Phe Pro Thr Thr Pro Ala Ala Val
 115 120 125

Asp Ala Leu Lys Pro Thr Arg Val Ile Lys Val
 130 135

<210> 56
 <211> 1272
 <212> DNA
 <213> Zea mays

<220>
 <221> exon
 <222> (3)..(185)
 <223> partial

<220>
 <221> Intron
 <222> (186)..(295)
 <223>

<220>
 <221> exon
 <222> (296)..(1066)
 <223>

<220>
 <221> 3'UTR
 <222> (1067)..(1272)
 <223>

<400> 56
 at gac gtg gag caa aac gat gat ctg tct gat tcc tct gtt gaa tct 47
 Asp Val Glu Gln Asn Asp Asp Leu Ser Asp Ser Ser Val Glu Ser
 1 5 10 15
 ttg cct gga atg gag att tct cca gat gat gtt gtc agt gct att ggt 95
 Leu Pro Gly Met Glu Ile Ser Pro Asp Asp Val Val Ser Ala Ile Gly
 20 25 30
 ccc aag cat ttt tgg aaa gcg aga aga gct att gtc aat cag cag agg 143
 Pro Lys His Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln Arg
 35 40 45
 gta ttt gct gtt caa gta ttc gag ctg cat agg ttg atc aaa 185
 Val Phe Ala Val Gln Val Phe Glu Leu His Arg Leu Ile Lys
 50 55 60
 gtgagtcctgc ggcaaataaa tataacttct ttgggcccat gcttatgggc aggttaattt 245
 aaatttgaaa awttgggttta acsgttgttt atgttgactt ttgcaatcag gtg cag 301
 Val Gln
 aag ttg atc gct gca tct cca cat gta ctt att gag ggg gat cct tgc 349
 Lys Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Gly Asp Pro Cys
 65 70 75
 ctt ggc aaa tcc ttg gcg gtg agc aag aaa agg ctg gct gga gat gtg 397
 Leu Gly Lys Ser Leu Ala Val Ser Lys Lys Arg Leu Ala Gly Asp Val
 80 85 90 95
 gaa aca cag ctt gaa tca gct aaa aac gat gat ggc gtg cga cca acg 445

Glu Thr Gln Leu Glu Ser Ala Lys Asn Asp Asp Gly Val Arg Pro Thr	
100 105 110	
cag cta gag cac tcg aaa gag aag act gaa gcg aac caa cct tca cca	493
Gln Leu Glu His Ser Lys Glu Lys Thr Glu Ala Asn Gln Pro Ser Pro	
115 120 125	
tct caa gac gaa cag gcc gca act aat ggt gac gtt gct gcc ttg atg	541
Ser Gln Asp Glu Gln Ala Ala Thr Asn Gly Asp Val Ala Ala Leu Met	
130 135 140	
cat acc cct tcc gac aac aaa cag aag agc tgg tgc att cct gca cct	589
His Thr Pro Ser Asp Asn Lys Gln Lys Ser Trp Cys Ile Pro Ala Pro	
145 150 155	
cca agt cag tgg ctg att cct gtw atg tcc ccg tct gaa gga ctt gtc	637
Pro Ser Gln Trp Leu Ile Pro Xaa Met Ser Pro Ser Glu Gly Leu Val	
160 165 170 175	
tac aag cct tat acc ggg cac tgc cct ccg gtg gga agt ctt ttg gcg	685
Tyr Lys Pro Tyr Thr Gly His Cys Pro Pro Val Gly Ser Leu Leu Ala	
180 185 190	
ccc cca ttt ttt gcc agc tac ccc acc tcc tcc tcc tcc aca gct ggg	733
Pro Pro Phe Phe Ala Ser Tyr Pro Thr Ser Ser Ser Ser Thr Ala Gly	
195 200 205	
ggg gat ttc atg agt tcg gca tgt gga gcc agg ctg atg agt gcc cct	781
Gly Asp Phe Met Ser Ser Ala Cys Gly Ala Arg Leu Met Ser Ala Pro	
210 215 220	
gtg tac ttc ccg tct ttc agc atg cct gca gtg tca ggg tct gca gtt	829
Val Tyr Phe Pro Ser Phe Ser Met Pro Ala Val Ser Gly Ser Ala Val	
225 230 235	
gag caa gtg agc cat gtt gca gcg tcg cag cat aaa cgg aac tcg tgt	877
Glu Gln Val Ser His Val Ala Ala Ser Gln His Lys Arg Asn Ser Cys	
240 245 250 255	
agt gaa gcg gtg ttg gca tca agg gac agc gag gtg caa ggc agt agt	925
Ser Glu Ala Val Leu Ala Ser Arg Asp Ser Glu Val Gln Gly Ser Ser	
260 265 270	
gct agc agt ccg gca tct tct gaa aca gca gct caa ccc agg gtc att	973
Ala Ser Ser Pro Ala Ser Ser Glu Thr Ala Ala Gln Pro Arg Val Ile	
275 280 285	
agg gtt gtt ccc cac acg gca cgc acg gct tca gag tcg gca gca agg	1021
Arg Val Val Pro His Thr Ala Arg Thr Ala Ser Glu Ser Ala Ala Arg	
290 295 300	
att ttc cgc tca ata cag atg gag agg aaa caa aac gac ccg tga	1066
Ile Phe Arg Ser Ile Gln Met Glu Arg Lys Gln Asn Asp Pro	
305 310 315	
ctggcagata aaaatgaaag aacggaggga gtagactaat tttttgaccg ataattataa	1126

tgatcgccgt aaattggctg gcccgccgc cttatgtttt ttgttcagtg taaatatgct 1186
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 tggaattaaa aaaaaaaaaa aaaaaa 1272

<210> 57
 <211> 317
 <212> PRT
 <213> Zea mays

<400> 57

Asp Val Glu Gln Asn Asp Asp Leu Ser Asp Ser Ser Val Glu Ser Leu
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Pro Gly Met Glu Ile Ser Pro Asp Asp Val Val Ser Ala Ile Gly Pro
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Lys His Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln Arg Val
 35 40 45

Phe Ala Val Gln Val Phe Glu Leu His Arg Leu Ile Lys Val Gln Lys
 50 55 60

Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Gly Asp Pro Cys Leu
 65 70 75 80

Gly Lys Ser Leu Ala Val Ser Lys Lys Arg Leu Ala Gly Asp Val Glu
 85 90 95

Thr Gln Leu Glu Ser Ala Lys Asn Asp Asp Gly Val Arg Pro Thr Gln
 100 105 110

Leu Glu His Ser Lys Glu Lys Thr Glu Ala Asn Gln Pro Ser Pro Ser
 115 120 125

Gln Asp Glu Gln Ala Ala Thr Asn Gly Asp Val Ala Ala Leu Met His
 130 135 140

Thr Pro Ser Asp Asn Lys Gln Lys Ser Trp Cys Ile Pro Ala Pro Pro
 145 150 155 160

Ser Gln Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr
 165 170 175

Lys Pro Tyr Thr Gly His Cys Pro Pro Val Gly Ser Leu Leu Ala Pro
 180 185 190

Pro Phe Phe Ala Ser Tyr Pro Thr Ser Ser Ser Ser Thr Ala Gly Gly
 195 200 205

Asp Phe Met Ser Ser Ala Cys Gly Ala Arg Leu Met Ser Ala Pro Val
 210 215 220

Tyr Phe Pro Ser Phe Ser Met Pro Ala Val Ser Gly Ser Ala Val Glu
 225 230 235 240

Gln Val Ser His Val Ala Ala Ser Gln His Lys Arg Asn Ser Cys Ser
 245 250 255

Glu Ala Val Leu Ala Ser Arg Asp Ser Glu Val Gln Gly Ser Ser Ala
 260 265 270

Ser Ser Pro Ala Ser Ser Glu Thr Ala Ala Gln Pro Arg Val Ile Arg
 275 280 285

Val Val Pro His Thr Ala Arg Thr Ala Ser Glu Ser Ala Ala Arg Ile
 290 295 300

Phe Arg Ser Ile Gln Met Glu Arg Lys Gln Asn Asp Pro
 305 310 315

<210> 58
 <211> 1980
 <212> DNA
 <213> Lycopersicon esculentum

<220>
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 <222> (2)..(1804)
 <223> portion of exon 1, exon 2, exon 3, and exon 4, including stop cod
 on

<220>
 <221> 3'UTR
 <222> (1085)..(1980)
 <223> partial

<400> 58
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1				5				10						15		
act	tca	aag	atg	gcc	cct	cca	tcc	tca	agc	cag	ggg	agt	ggg	cat	gac	97
Thr	Ser	Lys	Met	Ala	Pro	Pro	Ser	Ser	Ser	Gln	Gly	Ser	Gly	His	Asp	
			20				25						30			
aga	agt	gga	tat	ctc	cct	ata	caa	cac	cct	cca	tct	aga	cgt	cta	gct	145
Arg	Ser	Gly	Tyr	Leu	Pro	Ile	Gln	His	Pro	Pro	Ser	Arg	Arg	Leu	Ala	
		35					40					45				
gat	aaa	cca	cct	ggc	cac	agt	tcc	gat	ccc	agt	act	ctc	ttg	caa	caa	193
Asp	Lys	Pro	Pro	Gly	His	Ser	Ser	Asp	Pro	Ser	Thr	Leu	Leu	Gln	Gln	
	50					55					60					
tat	gaa	ttg	aaa	aag	aga	aca	gaa	gag	gat	gac	ttt	acg	gtc	ccc	atc	241
Tyr	Glu	Leu	Lys	Lys	Arg	Thr	Glu	Glu	Asp	Asp	Phe	Thr	Val	Pro	Ile	
65					70				75					80		
ttt	gtt	aat	tcc	aag	ctc	ggc	cag	gcc	cat	ggg	agt	cat	aat	gtg	aat	289
Phe	Val	Asn	Ser	Lys	Leu	Gly	Gln	Ala	His	Gly	Ser	His	Asn	Val	Asn	
			85					90						95		
atg	gaa	aag	ctc	tca	ccc	tct	ggc	caa	ctg	ttt	tgt	cct	aat	aaa	gag	337
Met	Glu	Lys	Leu	Ser	Pro	Ser	Gly	Gln	Leu	Phe	Cys	Pro	Asn	Lys	Glu	
			100				105						110			
ttg	gaa	gga	gtt	aca	cat	cta	aca	ttg	aga	caa	cag	cgc	aat	agc	caa	385
Leu	Glu	Gly	Val	Thr	His	Leu	Thr	Leu	Arg	Gln	Gln	Arg	Asn	Ser	Gln	
		115					120					125				
aac	aag	gag	aat	ctc	aaa	tgt	act	ctt	gct	cgt	aga	gag	aaa	aca	acc	433
Asn	Lys	Glu	Asn	Leu	Lys	Cys	Thr	Leu	Ala	Arg	Arg	Glu	Lys	Thr	Thr	
	130					135					140					
tca	aac	tct	gca	tcc	aag	gaa	tgc	aga	ttg	gat	cct	cag	gtt	ggc	tgt	481
Ser	Asn	Ser	Ala	Ser	Lys	Glu	Cys	Arg	Leu	Asp	Pro	Gln	Val	Gly	Cys	
145					150				155					160		
agt	agc	ata	cct	gaa	cct	gtt	aag	gga	aca	tat	gat	ggc	agt	tcg	tat	529
Ser	Ser	Ile	Pro	Glu	Pro	Val	Lys	Gly	Thr	Tyr	Asp	Gly	Ser	Ser	Tyr	
			165					170						175		
cct	agg	aaa	gaa	ttt	gta	tca	taa	gag	cag	tta	act	gct	aat	gat	ctt	577
Pro	Arg	Lys	Glu	Phe	Val	Ser		Glu	Gln	Leu	Thr	Ala	Asn	Asp	Leu	
			180					185						190		
gtt	aat	gat	acg	gaa	tcc	cag	gaa	gac	agg	gca	cac	aaa	tca	tta	caa	625
Val	Asn	Asp	Thr	Glu	Ser	Gln	Glu	Asp	Arg	Ala	His	Lys	Ser	Leu	Gln	
			195				200						205			
aca	gga	aat	ttg	gac	cga	ggc	gac	gac	tta	tct	gag	act	tcc	aga	gtg	673
Thr	Gly	Asn	Leu	Asp	Arg	Gly	Asp	Asp	Leu	Ser	Glu	Thr	Ser	Arg	Val	
		210					215					220				
gaa	tct	att	tct	gga	aca	gac	atc	tct	cct	gat	gac	att	gta	gga	ata	721
Glu	Ser	Ile	Ser	Gly	Thr	Asp	Ile	Ser	Pro	Asp	Asp	Ile	Val	Gly	Ile	

225	230	235	
att ggc tta aag cgt ttc tgg aaa gcc aga aga gca att gtc aac cag Ile Gly Leu Lys Arg Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln 240 245 250 255			769
caa aga gtg ttt gca atc caa gtg ttc gag ttg cat cga cta ata aag Gln Arg Val Phe Ala Ile Gln Val Phe Glu Leu His Arg Leu Ile Lys 260 265 270			817
gta caa agg ctc att gcc ggg tca cca aat agt tcg ctc gaa gat cct Val Gln Arg Leu Ile Ala Gly Ser Pro Asn Ser Ser Leu Glu Asp Pro 275 280 285			865
gct tat tta ggc aaa cct tta aag agt tca tcg atc aaa aga ctt cca Ala Tyr Leu Gly Lys Pro Leu Lys Ser Ser Ser Ile Lys Arg Leu Pro 290 295 300			913
ttg gac tgt att gtt aga gaa tct caa agt gtt ctg aag cgc aag cat Leu Asp Cys Ile Val Arg Glu Ser Gln Ser Val Leu Lys Arg Lys His 305 310 315			961
gat tct gag aag cct cac ttc agg atg gaa cac act gcc gaa agc aat Asp Ser Glu Lys Pro His Phe Arg Met Glu His Thr Ala Glu Ser Asn 320 325 330 335			1009
gtg gga aag gca tct ctc tct act gtg caa aat ggt agt caa ctc tct Val Gly Lys Ala Ser Leu Ser Thr Val Gln Asn Gly Ser Gln Leu Ser 340 345 350			1057
agc cac aaa cca ttt tca gga act cca ctg cct aca cct gta aca aat Ser His Lys Pro Phe Ser Gly Thr Pro Leu Pro Thr Pro Val Thr Asn 355 360 365			1105
gat tct aat gcg ggt cct tgg tgc ttc caa caa cct ccc ggg cac caa Asp Ser Asn Ala Gly Pro Trp Cys Phe Gln Gln Pro Pro Gly His Gln 370 375 380			1153
tgg ttg atc cca gtg atg tct cct tct gag gga ctt gta tac aag cca Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr Lys Pro 385 390 395			1201
ttt cct gga cct gga ttc acg agt cct att tgt gga agt ggg cct cca Phe Pro Gly Pro Gly Phe Thr Ser Pro Ile Cys Gly Ser Gly Pro Pro 400 405 410 415			1249
gga tcg agt cca aca atg ggg aac ttt ttt gct cca aca tat gga gtt Gly Ser Ser Pro Thr Met Gly Asn Phe Phe Ala Pro Thr Tyr Gly Val 420 425 430			1297
cct gct cct aat cct cac tat caa ggt atg gga gtt cct ttt gca cct Pro Ala Pro Asn Pro His Tyr Gln Gly Met Gly Val Pro Phe Ala Pro 435 440 445			1345
ccg act ggt cat ggt tac ttt cgg caa tat ggc atg cca gct atg aat Pro Thr Gly His Gly Tyr Phe Arg Gln Tyr Gly Met Pro Ala Met Asn 450 455 460			1393

cca cca att tca tca act gct agt gaa gaa tcg aac cag tat acc atg	1441
Pro Pro Ile Ser Ser Thr Ala Ser Glu Glu Ser Asn Gln Tyr Thr Met	
465 470 475	
cct ggt tta caa cac cag ttt tct gga gta gtt gat gac gtc aac att	1489
Pro Gly Leu Gln His Gln Phe Ser Gly Val Val Asp Asp Val Asn Ile	
480 485 490 495	
caa cat cag gac tca agt aat gtt cta aat cag aag aaa gaa aat gtc	1537
Gln His Gln Asp Ser Ser Asn Val Leu Asn Gln Lys Lys Glu Asn Val	
500 505 510	
ccg gat gtt gta agg tat caa tcc aca aaa gat aat gag gta caa gcc	1585
Pro Asp Val Val Arg Tyr Gln Ser Thr Lys Asp Asn Glu Val Gln Ala	
515 520 525	
agc agt gca agt agt cct att gag aca gca gga aga aac atg ctc tct	1633
Ser Ser Ala Ser Ser Pro Ile Glu Thr Ala Gly Arg Asn Met Leu Ser	
530 535 540	
ctt ttt ccc acg tct cca gtt act gac aac cgt gat ggt agc cct cag	1681
Leu Phe Pro Thr Ser Pro Val Thr Asp Asn Arg Asp Gly Ser Pro Gln	
545 550 555	
gct tgt gtg cct gat aat cca gcc aga gtt atc aag gtt gta cct cac	1729
Ala Cys Val Pro Asp Asn Pro Ala Arg Val Ile Lys Val Val Pro His	
560 565 570 575	
aat gca agg tct gct aca gaa tcc gta gct cgg ata ttt cag tct ata	1777
Asn Ala Arg Ser Ala Thr Glu Ser Val Ala Arg Ile Phe Gln Ser Ile	
580 585 590	
caa caa gag aga aat aat atg act tag gtttaacaca tctataagta	1824
Gln Gln Glu Arg Asn Asn Met Thr	
595	
gcttaccttg tgaatatgac catttgctca tcctggcaaa atgtagtagt ttcagtc	1884
aat	
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tagataagca tacctgcaaa aaaaaaaaaa aaaaac	1980

<210> 59
 <211> 599
 <212> PRT
 <213> Lycopersicum esculentum

<400> 59

Pro Ser Gln Arg Phe Asn Ser Gly Val Leu Pro Leu Asp Pro Asn Asn
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Thr Ser Lys Met Ala Pro Pro Ser Ser Gln Gly Ser Gly His Asp
20 25 30

Arg Val Phe Ala Ile Gln Val Phe Glu Leu His Arg Leu Ile Lys Val
260 265 270

Gln Arg Leu Ile Ala Gly Ser Pro Asn Ser Ser Leu Glu Asp Pro Ala
275 280 285

Tyr Leu Gly Lys Pro Leu Lys Ser Ser Ser Ile Lys Arg Leu Pro Leu
290 295 300

Asp Cys Ile Val Arg Glu Ser Gln Ser Val Leu Lys Arg Lys His Asp
305 310 315 320

Ser Glu Lys Pro His Phe Arg Met Glu His Thr Ala Glu Ser Asn Val
325 330 335

Gly Lys Ala Ser Leu Ser Thr Val Gln Asn Gly Ser Gln Leu Ser Ser
340 345 350

His Lys Pro Phe Ser Gly Thr Pro Leu Pro Thr Pro Val Thr Asn Asp
355 360 365

Ser Asn Ala Gly Pro Trp Cys Phe Gln Gln Pro Pro Gly His Gln Trp
370 375 380

Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr Lys Pro Phe
385 390 395 400

Pro Gly Pro Gly Phe Thr Ser Pro Ile Cys Gly Ser Gly Pro Pro Gly
405 410 415

Ser Ser Pro Thr Met Gly Asn Phe Phe Ala Pro Thr Tyr Gly Val Pro
420 425 430

Ala Pro Asn Pro His Tyr Gln Gly Met Gly Val Pro Phe Ala Pro Pro
435 440 445

Thr Gly His Gly Tyr Phe Arg Gln Tyr Gly Met Pro Ala Met Asn Pro
450 455 460

Pro Ile Ser Ser Thr Ala Ser Glu Glu Ser Asn Gln Tyr Thr Met Pro
465 470 475 480

Gly Leu Gln His Gln Phe Ser Gly Val Val Asp Asp Val Asn Ile Gln
485 490 495

His Gln Asp Ser Ser Asn Val Leu Asn Gln Lys Lys Glu Asn Val Pro
500 505 510

Asp Val Val Arg Tyr Gln Ser Thr Lys Asp Asn Glu Val Gln Ala Ser
515 520 525

Ser Ala Ser Ser Pro Ile Glu Thr Ala Gly Arg Asn Met Leu Ser Leu
530 535 540

Phe Pro Thr Ser Pro Val Thr Asp Asn Arg Asp Gly Ser Pro Gln Ala
545 550 555 560

Cys Val Pro Asp Asn Pro Ala Arg Val Ile Lys Val Val Pro His Asn
565 570 575

Ala Arg Ser Ala Thr Glu Ser Val Ala Arg Ile Phe Gln Ser Ile Gln
580 585 590

Gln Glu Arg Asn Asn Met Thr
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<210> 60
<211> 1972
<212> DNA
<213> Brassica sp.

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<223> partial

<220>
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<222> (344)..(792)
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<222> (1505)..(1556)
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<222> (1649)..(1972)
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 <222> (148)..(343)
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<400> 60
 aaa gga gga gga cct cga gct cct cct aga aac aag atg gct ctc tac 48
 Lys Gly Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met Ala Leu Tyr
 1 5 10 15

gag cac ctc acc acc cct tct cac agg ttt act gat cat agt tcc tcg 96
 Glu His Leu Thr Thr Pro Ser His Arg Phe Thr Asp His Ser Ser Ser
 20 25 30

cca cgt cac acc aac act ctc ttt cct cct cct cct gga cca tct aac 144
 Pro Arg His Thr Asn Thr Leu Phe Pro Pro Pro Pro Gly Pro Ser Asn
 35 40 45

cag gtactactga gtttttagta ataatatata ttagttacag caaatcttaa 197
 Gln

tttcttgctg tgtcttatta ccatggttcg tttgtggaaa tgattatctt ttaaagctat 257

aaccttcttg ttatgctgaa tagtttcagt agaagattat atagtgtatg tgggacattg 317

gaaataatta tcttttttatt ctgcag cct tgt ggg gtg gag aga aac ttg act 370
 Pro Cys Gly Val Glu Arg Asn Leu Thr
 50 55

tcc cag cat ctt gat tct tca gct tct ggc cat gta acc caa atg tcc 418
 Ser Gln His Leu Asp Ser Ser Ala Ser Gly His Val Thr Gln Met Ser
 60 65 70

tcc atg gaa aat gtg aca act tta gca cat cgt cgt ggt gat caa agg 466
 Ser Met Glu Asn Val Thr Thr Leu Ala His Arg Arg Gly Asp Gln Arg
 75 80 85 90

aaa acg cta aga gag gaa gat gat ttt gcg gtt cct gta tat gtt aat 514
 Lys Thr Leu Arg Glu Glu Asp Asp Phe Ala Val Pro Val Tyr Val Asn

95	100	105	
gat agc tca aga aga ttt caa tgt cct ctt gaa aag tca gca tcg ggt Asp Ser Ser Arg Arg Phe Gln Cys Pro Leu Glu Lys Ser Ala Ser Gly 110 115 120			562
tgt gaa aga gtt aat gct tct tgt gag aca gag tct aca agt agt agg Cys Glu Arg Val Asn Ala Ser Cys Glu Thr Glu Ser Thr Ser Ser Arg 125 130 135			610
tta gac cat gaa act gga gtg atg gaa act gat gat gga gtt gaa tct Leu Asp His Glu Thr Gly Val Met Glu Thr Asp Asp Gly Val Glu Ser 140 145 150			658
cat ggc aat cct aat gac gtc gat gat gat gat gat gat tcg ata His Gly Asn Pro Asn Asp Val Asp Asp Asp Asp Asp Asp Ser Ile 155 160 165 170			706
tcc agc ata gac gtc tct tct gat gaa gtt gtg gga gta tta ggt caa Ser Ser Ile Asp Val Ser Ser Asp Glu Val Val Gly Val Leu Gly Gln 175 180 185			754
aac cgk ttc tgg aga gca agg aar gct atk gcc aag aa gtyccata Asn Arg Phe Trp Arg Ala Arg Lys Ala Xaa Ala Lys Asn 190 195			802
gacttttggt gaactggttaa ggaatttttt gggcttttct ctgctgtttt aatgcttaaa			862
tgatgcaatg gtttgctcac aacatacata tatgattata actctgcttt atattttgaa			922
aaagaccaga tttggtttat ttttgattga gaagtataa ttttttagtg aagaaacccc			982
ctgactcctc caaaaattga aggttcccgc cgagacagtt aatggatttt gcatctgctt			1042
gctggaacat gtccctgtcc ctgtctcggt ttggtatttg cttttattct gcattttccc			1102
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cataatgtct tcagtttttc ttcttctatt atttatgcct ttctctgtgt tttttgacgc			1342
attgatttgc ttcttcatca ttgttggtta gaggttctt gcttcttttt ttttccgatt			1402
ctactgttct attatttggt caaccgaaac tatatctatc tctctttgtg gaacttttct			1462
tatgggtcat cttcttgatc tgaccttggt tctccgtaac ag t caa caa aga ata Gln Gln Arg Ile 200			1517
ttt gcg gtt caa tta ttt gag ttg cac agg ctr att aag gtaaaactca Phe Ala Val Gln Leu Phe Glu Leu His Arg Xaa Ile Lys 205 210 215			1566
ttcagaaaac ttctcctacg tttcatgaat atttgttttg tgcaaacctg gtcaactgta			1626

ctttgttttc actataatca ag gtt caa aga ctt att gct tca tca tcg gat	1678
Val Gln Arg Leu Ile Ala Ser Ser Ser Asp	
220 225	
gtc ttg ctc gat gag atc agt tat ctt gga aat gtt cca gtg aag aag	1726
Val Leu Leu Asp Glu Ile Ser Tyr Leu Gly Asn Val Pro Val Lys Lys	
230 235 240	
ctt ctt ccc tct gaa ttt ata tta aag cct cct cct cta cca cag gtt	1774
Leu Leu Pro Ser Glu Phe Ile Leu Lys Pro Pro Pro Leu Pro Gln Val	
245 250 255	
acc aaa cac aga agc agc gac tcc gag aag act gac caa aat aaa atg	1822
Thr Lys His Arg Ser Ser Asp Ser Glu Lys Thr Asp Gln Asn Lys Met	
260 265 270	
gaa tcc tca gct gag aac gta gtc ggg aag tcg tca aac caa ggt cag	1870
Glu Ser Ser Ala Glu Asn Val Val Gly Lys Ser Ser Asn Gln Gly Gln	
275 280 285 290	
cag cat caa ccg tcc aac tac atg cct ttt gcg agc aac cca cca gct	1918
Gln His Gln Pro Ser Asn Tyr Met Pro Phe Ala Ser Asn Pro Pro Ala	
295 300 305	
gca aat gga tgt tac tat cct cct cag cat cct cct ccc tct gga gga	1966
Ala Asn Gly Cys Tyr Tyr Pro Pro Gln His Pro Pro Pro Ser Gly Gly	
310 315 320	
aat cag	1972
Asn Gln	

<210> 61
 <211> 324
 <212> PRT
 <213> Brassica sp.

<220>
 <221> misc_feature
 <222> (188)..(188)
 <223> Xaa = uncertain amino acid residue

<220>
 <221> misc_feature
 <222> (194)..(194)
 <223> Xaa = uncertain amino acid residue

<220>
 <221> misc_feature
 <222> (196)..(196)
 <223> Xaa = uncertain amino acid residue

<220>
 <221> misc_feature
 <222> (214)..(214)
 <223> Xaa = uncertain amino acid residue

<400> 61

Lys Gly Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met Ala Leu Tyr
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Glu His Leu Thr Thr Pro Ser His Arg Phe Thr Asp His Ser Ser Ser
 20 25 30

Pro Arg His Thr Asn Thr Leu Phe Pro Pro Pro Pro Gly Pro Ser Asn
 35 40 45

Gln Pro Cys Gly Val Glu Arg Asn Leu Thr Ser Gln His Leu Asp Ser
 50 55 60

Ser Ala Ser Gly His Val Thr Gln Met Ser Ser Met Glu Asn Val Thr
 65 70 75 80

Thr Leu Ala His Arg Arg Gly Asp Gln Arg Lys Thr Leu Arg Glu Glu
 85 90 95

Asp Asp Phe Ala Val Pro Val Tyr Val Asn Asp Ser Ser Arg Arg Phe
 100 105 110

Gln Cys Pro Leu Glu Lys Ser Ala Ser Gly Cys Glu Arg Val Asn Ala
 115 120 125

Ser Cys Glu Thr Glu Ser Thr Ser Ser Arg Leu Asp His Glu Thr Gly
 130 135 140

Val Met Glu Thr Asp Asp Gly Val Glu Ser His Gly Asn Pro Asn Asp
 145 150 155 160

Val Asp Asp Asp Asp Asp Asp Ser Ile Ser Ser Ile Asp Val Ser
 165 170 175

Ser Asp Glu Val Val Gly Val Leu Gly Gln Asn Xaa Phe Trp Arg Ala
 180 185 190

Arg Xaa Ala Xaa Ala Lys Asn Gln Gln Arg Ile Phe Ala Val Gln Leu

195	200	205
Phe Glu Leu His Arg Xaa Ile Lys Val Gln Arg Leu Ile Ala Ser Ser 210 215 220		
Ser Asp Val Leu Leu Asp Glu Ile Ser Tyr Leu Gly Asn Val Pro Val 225 230 235 240		
Lys Lys Leu Leu Pro Ser Glu Phe Ile Leu Lys Pro Pro Pro Leu Pro 245 250 255		
Gln Val Thr Lys His Arg Ser Ser Asp Ser Glu Lys Thr Asp Gln Asn 260 265 270		
Lys Met Glu Ser Ser Ala Glu Asn Val Val Gly Lys Ser Ser Asn Gln 275 280 285		
Gly Gln Gln His Gln Pro Ser Asn Tyr Met Pro Phe Ala Ser Asn Pro 290 295 300		
Pro Ala Ala Asn Gly Cys Tyr Tyr Pro Pro Gln His Pro Pro Pro Ser 305 310 315 320		

Gly Gly Asn Gln

<210> 62
 <211> 505
 <212> DNA
 <213> Brassica

<220>
 <221> exon
 <222> (2)..(505)
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cct cct ccg ttt cac ccg ggc atg gga ttc cya tct cat ggt aat ggc Pro Pro Pro Phe His Pro Gly Met Gly Phe Xaa Ser His Gly Asn Gly	145

35	40	45	
tac ttt cct cca tat ggt ggt atc atg atg aac cct tac tat tcc gga			193
Tyr Phe Pro Pro Tyr Gly Gly Ile Met Met Asn Pro Tyr Tyr Ser Gly			
50	55	60	
cra caa caa caa caa caa ccc aat gag caa atg aac aac aac atc caa			241
Xaa Gln Gln Gln Gln Gln Pro Asn Glu Gln Met Asn Asn Asn Ile Gln			
65	70	75	80
caa cag agc tca gtg aat gaa gcg act tca caa caa caa cag cca acg			289
Gln Gln Ser Ser Val Asn Glu Ala Thr Ser Gln Gln Gln Gln Pro Thr			
	85	90	95
aaa tct tat cct cgg gct aaa aag agc agg caa gag gga atc tct ggt			337
Lys Ser Tyr Pro Arg Ala Lys Lys Ser Arg Gln Glu Gly Ile Ser Gly			
	100	105	110
aag aag aag tcc ttt caa cca ttc tca gcg gtt gat gat gtt cat gat			385
Lys Lys Lys Ser Phe Gln Pro Phe Ser Ala Val Asp Asp Val His Asp			
	115	120	125
gac aag atc aac aat gct gca caa cct act gag gaa atg atg acg aca			433
Asp Lys Ile Asn Asn Ala Ala Gln Pro Thr Glu Glu Met Met Thr Thr			
	130	135	140
acc aca acc aca aca aca act gtg act cag aca acg aga gat gga gca			481
Thr Thr Thr Thr Thr Thr Thr Val Thr Gln Thr Thr Arg Asp Gly Ala			
	145	150	155
			160
gga gtg acg aga gtg atc aag gtg			505
Gly Val Thr Arg Val Ile Lys Val			
	165		

<210> 63
 <211> 168
 <212> PRT
 <213> Brassica sp.

<220>
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 <223> Xaa = uncertain amino acid residue

<220>
 <221> misc_feature
 <222> (65)..(65)
 <223> Xaa = uncertain amino acid residue

<400> 63

Pro Gly Pro Asp Pro Gly His Thr Gly Pro Val Cys Gly Gly Tyr Tyr
1 5 10 15

Gly His Phe Met Pro Ala Pro Met Phe Met Gly Gly Gly Gly Gly Gln
 20 25 30

Pro Pro Pro Phe His Pro Gly Met Gly Phe Xaa Ser His Gly Asn Gly
 35 40 45

Tyr Phe Pro Pro Tyr Gly Gly Ile Met Met Asn Pro Tyr Tyr Ser Gly
 50 55 60

Xaa Gln Gln Gln Gln Gln Pro Asn Glu Gln Met Asn Asn Asn Ile Gln
 65 70 75 80

Gln Gln Ser Ser Val Asn Glu Ala Thr Ser Gln Gln Gln Gln Pro Thr
 85 90 95

Lys Ser Tyr Pro Arg Ala Lys Lys Ser Arg Gln Glu Gly Ile Ser Gly
 100 105 110

Lys Lys Lys Ser Phe Gln Pro Phe Ser Ala Val Asp Asp Val His Asp
 115 120 125

Asp Lys Ile Asn Asn Ala Ala Gln Pro Thr Glu Glu Met Met Thr Thr
 130 135 140

Thr Thr Thr Thr Thr Thr Thr Val Thr Gln Thr Thr Arg Asp Gly Ala
 145 150 155 160

Gly Val Thr Arg Val Ile Lys Val
 165

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 <211> 36
 <212> DNA
 <213> synthetic oligonucleotide

<220>
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 <222> (28)..(28)
 <223> n = any nucleic acid residue

<400> 64
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36

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 <223> n = any nucleic acid

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 <213> synthetic oligonucleotide

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 <400> 66
 caaagagttt ttgctgttca agttttygar ytnca 35

 <210> 67
 <211> 20
 <212> DNA
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 <400> 67
 tcaatcagtc acctgggcat 20

 <210> 68
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 <212> DNA
 <213> synthetic oligonucleotide

 <220>
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 <223> n = any nucleic acid

 <400> 68
 cartggytnr ttctgttat gtctccttct gaagg 35